protein

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Run on:

Appli Appli

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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     June 28, 2002, 07:41:41; Search time 43.94 Seconds (without alignments) 90.053 Million cell updates/sec
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MRSSPGNMERIVICLMVIFL.....LLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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US-09-522-217-2
US-09-522-217-85
US-09-522-217-89
US-09-522-217-89
US-09-522-217-72
US-08-031-399-6
US-08-031-399-12
US-08-393-305-3
US-08-726-817-3
US-08-725-969-3
US-08-725-969-2
US-08-725-22-217-113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
Sequence 2, Appli
Sequence 89, Appl
Sequence 89, Appli
Sequence 73, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 3, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 2, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                   Description
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                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: NO. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Holly, Richard D.
APPLICANT: Obliston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hollon, Stacey R.
APPLICANT: Hollon, Stacey R.
APPLICANT: Hommond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Homo
US-09-522-217-2
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US-09-522-217-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/09522217 Patent No. 6307024 GENERAL INFORMATION:
                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 162; Conserv
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                                                                                                                                                         1 MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
                                                                             LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
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                                    TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                          MRSSPGNMERIVICLMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEF
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PCT-US96-06423-2

US-08-031-399-3

US-08-393-305-6

US-08-726-817-6

US-08-725-969-6

US-08-725-969-6

US-08-794-524-6

US-09-189-193-3

US-08-300-903A-3

US-08-301-399-2

US-08-393-305-5

US-08-284-393B-9

US-08-284-393B-9

US-08-725-969-5

US-08-725-969-5
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pred. No. 4.8e-87;
pred. No. 4.8e-87;
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Sequence
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Result

No

Score

Match

Length

DB

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224.9 211.7 111.7 111.7 111.7 111.7 111.7 111.7 111.7 111.7 111.7 111.7 111.7 111.7

0;

Gaps

0;

60 60 Minimum Maximum

DB

length: 0 length: 2000000000

Post-processing:

Minimum Match

Scoring table: Sequence: Title: Perfect score:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

US-09-825-561A-10 850

Searched:

231628 seqs,

tal number

Database

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,

US-09-522-217-85

Sequence 85, Application US/09522217 Patent No. 6307024

INFORMATION:

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Sequence 56, Application US/09522217

Patent No. 6307024

GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nolnston, Janet V.
APPLICANT: Billon, Stacey R.
APPLICANT: Hammond, Angela K.
APPLICANT: Hammond, Angela K.
FIILE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER EILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SEQ ID NO 85
SEQ ID NO 85
LENGTH 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Foster, Donald C.
APPLICANT: Gross, Jane A.
APPLICANT: Holly, Richard D.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hollon, Stacey R.
APPLICANT: Hollon, Stacey R.
APPLICANT: Hommond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
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OTHER INFORMATION: MBP-human zalphall Ligand fusion polypeptide
US-09-522-217-85
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Best Local Similarity 95.7
Matches 134; Conservative
CURRENT FILING DATE: 2000-03-09
                     CURRENT APPLICATION NUMBER: US/09/522,217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  500 LLQKMIHQHLSSRTHGSEDS 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 LLQKMIHQHLSSRTHGSEDS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  383 LVPRGS---QDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23 LVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKA 82
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95.7%;
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Pred. No. 3.3e-69;
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33 DRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNN 92

Conservative

19;

Mismatches

Indels

0,

Gaps

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; ORGANISM: Artificial Sequence
; PEATURE:
; OTHER INFORMATION: MBP-mouse zalphall Ligand fusion polypeptide
US-09-522-217-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Uniston, Janet V.
APPLICANT: Uniston, Andrew J.
APPLICANT: Billon, Stacey R.
APPLICANT: Hollon, Stacey R.
APPLICANT: Hommond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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US-09-522-217-89
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                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-10
EARLIER FILING DATE: 1999-07-01
                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 89
Matches
                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 89,
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Best Local
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EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER: OF SEQ ID NOS: 115
                                                                                                                                                                                    LENGTH: 51
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11 Similarity 63.0%; 92; Conservative 2:
                                                                                                                                                                                                          510
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                  46.4%; Score 394; DB 4; 62.0%; Pred. No. 1.1e-35;
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Pred. No. 1.2e-46;
3; Mismatches 31
                               Length 510
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GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Hammond, Angela K.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/522/217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-10
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-07-01
NUMBER: OF SEQ ID NOS: 115
SOFTWARE: FASTUSED for Windows Version 3.0
SEQ ID NO 72
LENGTH: 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NO. 6307024aK, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIGAND FILE REFERENCE: 99-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-522-217-72

; Sequence 72, Appli

; Patent No. 6307024
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; Sequence 73, Application US/09522217

; Patent No. 6307024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: HuzalphallL-1 peptide US-09-522-217-72
                                                                                                                                                                                                                                                                                                                                                                                   Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     153 S 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ilarity 100
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9%; Score 212; DB 4;
100.0%; Pred. No. 6.9e-17;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-07-01
NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER: FastSED for Windows Version 3.0
SED ID NO 73
SED ID NO 73
LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: HuzalphallL-3 peptide US-09-522-217-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
US-08-031-399-6
                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NOTA:
APPLICATION NOTA:
APPLICATION UNMBER: US/08/031,399
FILING DATE: 1993030
CLASSIFICATION: 530
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, App
Patent No. 555
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Best Local Similarity
Matches 32; Conserv
                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 32
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Grabstein, Kenn
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Epithelium-derived T-cell Factor NUMBER OF SEQUENCES: 12
                                      TYPE: AMI
                                                          : 114 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08031399
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                                           linear
: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.7%; Score 176; DB 4;
100.0%; Pred. No. 5.2e-1;
tive 0; Mismatches
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TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-031-399-12
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  US-08-393-305-3; Sequence 3, Ap
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AMAE: Launer, Charlene
REGISTRATION NUMBER: 33,035
REFERENCE/DOCKET NUMBER: 2811
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0430
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 12, Applicat
Patent No. 5552303
GENERAL INFORMATION:
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Best Local 9
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Best Local Similarity 25.2
Matches 30; Conservative
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MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIO Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/031,399
FILING DATE: 19390308
FLIANG DATE: 19390308
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Grabstein, Kenneth APPLICANT: Anderson, Dirk APPLICANT: Elseman, June APPLICANT: Elseman, June APPLICANT: Rauch, Charles APPLICANT: Rauch, Charles APPLICANT: Reuch, Charles TITLE OF INVENTION: Epithelium-derived T-cell Factor NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                       93 --ERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149 | ; | ; | ; | ; | ; | ; | ; | ; |
                                                                                                     62 TVENLITLANNXLSSNGNXTESG------CKECEELEEKNIKEFLQSFVHIVQMFIN 112
                                                                                                                                                                                                                        43 IDIVDOLKNYVNDLVPEE-----LPAPEDVETNCEWSAFSCF-QKAQLKSANTGNN---- 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              43 IDIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTANKCFLLELQVISXESGDXXIHD 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD 61
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    Application US/08393305
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                                                                                                                                                                                                                                                               11.7%; Score 99.5; DB 1; Length 114; 25.2%; Pred. No. 0.00086; vative 23; Mismatches 45; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.7%; Score 99.5; DB 1; Length 114; 25.9%; Pred. No. 0.00086; Vative 23; Mismatches 48; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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US-08-726-817-3
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                                                                                                                                                                                                                                                                                   Sequence 3, Application US/08726817
Patent NO. 5707616
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match 11.7%; Score 99.5; DB 1;
Best Local Similarity 25.9%; Pred. No. 0.00086;
Matches 30; Conservative 23; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 5574138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 206-622-49
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
COMPUTER READABLE FORM:
                                                                                                                                                                                                    APPLICANT: Fung, Victor APPLICANT: Rauch, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                               CITY:
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 COLUMN CITY: Seattle STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                        98104
                                                                                 Seattle
                                                          Washington
                                                                                                 E: Seed and Berry 6300 Columbia Cen
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206-622-4900
3:
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                                                                                                     Center,
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COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/393,305
FILING DATE: 22-FEB-1995
FILING DATE: 22-FEB-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D
REGISTRATION NUMBER: 33,963
REGISTRATION NUMBER: 480052.409C2 APPLICANT: Fung, Victor
APPLICANT: Fauch, Charles
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR 6300 Columbia Center, 701 Fifth Avenue Length 114;

43 IDIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE 93 62 TVENLII -- LANNSLSSNGNVTES -- - GCKECEELEEKNIKEFLQSFVHIVQMFIN 112 94 RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149 3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD 48; Indels 15; Gaps 61

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NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Born. 701 Fifth Avenue

MEDIUM TYPE:

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US-08-504-042-6
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FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: MCMASters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 4800
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
TYPE: amino acid
TOPOLOGY: line-
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Elseum....
APPLICANT: Fung, Victor
APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell Factor
TITLE OF STOURNCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,817
FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                              STREET: 51.
STREET: Seattle
CITY: Seattle
cTATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acid
                                                                                    FILING DATE: 19-JUL-1
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/504,042
                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                            APPLICATION NUMBER: US 0: FILING DATE: 08-MAR-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 TVENLII -- LANNSLSSNGNVTES---GCKECEELEEKNIKEFLQSFVHIVQMFIN 112
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Local Similarity 25.9%;
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                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD 61
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No. 5747024
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                                                                                                                                                                                                                                                                                    98101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08504042
                                                                                                                                                                                                                                                                                                                                                     51 University Street
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                           Immunex Corporation
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                                                                                                                                                                                                                                          Floppy disk
                                                                                                                             19-JUL-1995
                  Charlene
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                                                                      us 08/031,399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 99.5; DB 1; Pred. No. 0.00086;
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US-08-504-042-12
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; HYPOTHETICAL: US-08-504-042-12
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GENERAL INFORMATION:
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                               APPLICATION NUMBER: US/08/
FILING DATE: 19-JUL-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 08-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Launer, Charlene
REGISTRATION NUMBER: 33,03
                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 114 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acid
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TELECOMMUNICATION INFORMATION:
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HYPOTHETICAL:
                                                                                                                                                               REFERENCE/DOCKET NUMBER: 28 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Grabstein, Kenneth
APPLICANT: Anderson, Dirk
APPLICANT: Eisenman, June
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rauch, Charles
TITLE OF INVENTION: Epithelium-derived T-cell Factor
NUMBER OF SEQUENCES: 12
                                   MOLECULE TYPE:
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STREET: 51
                                               TYPE: amino aciu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43 IDIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF-----QKAQLKSANTGNNE 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94 RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149
                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD
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51 University Street
                                                                                        114 amino acids
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                            206-587-0430
SEO ID NO: 12:
                                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.7%; Score 99.5; DB 1; 25.9%; Pred. No. 0.00086;
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Length 114;

US-08-794-524-3

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US-08-725-969-3
RESULT
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/725,969
FILING DATE: 04-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 206-622-4900 INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 114 amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/393,305
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                   43 IDIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF-----QKAQLKSANTGNNE 93
                                                                                                                                                                                                        / Match 11.7%; score 99.5; DB 2;
Local Similarity 25.9%; Pred. No. 0.00086;
les 30; Conservative 23; Mismatches 48
                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
TOPOLOGY: linear
14
                                                     62 TVENLII--LANNSLSSNGNVTES---GCKECEELEEKNIKEFLQSFVHIVQMFIN 112
                                                                                       94 RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: McMasters, David D.
REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 480052.409C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                            3 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD 61
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Eisenman, June
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us/08/725,969
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                                                                                                                                                                                                                                             Length 114;
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RESULT 15
US-09-189-193-3
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Patent No. 6184359
GENERAL INFORMATION:
APPLICANT: Grabstein, Kenneth
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FILING DATE: 03-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/393,305
FILING DATE: 22-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMasters, David D.
REGISTRATION NUMBER: 480052.409C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 206-622-49
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and
                                                                                                              APPLICANT: Rauch, Charles
TITLE OF INVENTION: EPITHELIUM-DERIVED T-CELL FACTOR
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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LENGTH: 114 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 6300 Columl
CITY: Seattle
STATE: Washington
COUNTRY: USA
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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STREET:
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3: Seed and Berry
6300 Columbia Center, 701 Fifth Avenue
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206-023-4900
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CITY: Seattle

STATE: Washington

COUNTRY: USA

COMPUTER: INSAMELE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PAPLICATION NUMBER: US/09/189,193

FILING DATE: 22-FEB-195

FRIDE APPLICATION NUMBER: US/09/189,193

FILING DATE: 22-FEB-195

FATORNEY/AGENT INFORMATION:

PRIOR APPLICATION NUMBER: 30,963

REFERENCE/DOCKET NUMBER: 480052.409C2

TELECOMMUNICATION NUMBER: 39,963

REFERENCE/DOCKET NUMBER: 480052.409C2

TELECOMMUNICATION NUMBER: 39,963

REFERENCE/DOCKET NUMBER: 480052.409C2

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REFERENCE/DOCKET NUMBER: 480052.409C2

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3: /cgn2_6/ptodata/2
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                          Sequence 2, Appli Sequence 97, Appli Sequence 12, Appli Sequence 12, Appli Sequence 13, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 17, Appli Sequence 17, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 19, Appli Sequence 19, Appli Sequence 19, Appli Sequence 15, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli
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2 US-08-693-697-33 2 US-08-588-526-3 4 US-08-618-957A-8 1 US-08-355-888A-8 1 US-08-697-8 2 US-08-696-8 2 US-08-696-8 2 US-08-696-8 2 US-08-691-697-8 3 US-08-691-697-20 2 US-08-618-957A-3 4 US-08-1827-962-20 2 US-08-763-1	-08-693-697-33 Sequence -08-588-526-3 Sequence -08-588-526-3 Sequence -08-355-888A-8 Sequence -08-588-190-3 Sequence -08-640-389A-3 Sequence -08-640-389A-3 Sequence -08-640-389A-3 Sequence -08-640-389A-3 Sequence -08-693-696-8 Sequence -08-693-696-8 Sequence -08-184-224-2 Sequence -08-184-224-2 Sequence -08-184-327A-8 Sequence -08-184-327A-8 Sequence -08-184-327A-9 Sequence -08-184-327A-9 Sequence -08-184-327A-9 Sequence	626	482	482	382	382	369	369	1162	960	960	960	960	960	960	958	908	908	700
US-08-588-597-33 US-08-588-526-3 US-08-588-598-8 US-08-588-190-3 US-08-588-190-3 US-08-693-697-8 US-08-640-389A-3 US-08-484-327A-8 US-08-184-327A-8 US-08-184-327A-8 US-08-184-327A-2	-08-693-697-33 Sequence -08-588-526-3 Sequence -08-588-526-3 Sequence -08-355-888A-8 Sequence -08-588-190-3 Sequence -08-640-389A-3 Sequence -08-640-389A-3 Sequence -08-640-389A-3 Sequence -08-640-389A-3 Sequence -08-693-696-8 Sequence -08-693-696-8 Sequence -08-184-224-2 Sequence -08-184-224-2 Sequence -08-184-327A-8 Sequence -08-184-327A-8 Sequence -08-184-327A-9 Sequence -08-184-327A-9 Sequence -08-184-327A-9 Sequence	۲	5	- 4	N	N	Ŋ	Ν	4	4	w	N	2	N	H	4	N	N	4
		US-08-184-327A-2	PCT-US95-00670-8	US-08-184-327A-8	US-08-460-402-3	US-08-078-311-3	PCT-US94-02891-69	US-08-424-224-2	US-08-827-962-20	US-08-618-957A-3	US-08-693-696-8	US-08-640-389A-3	US-08-693-697-8	US-08-588-190-3	US-08-355-888A-8	US-08-618-957A-8	US-08-588-526-3	US-08-693-697-33	ON OU OIL STAN
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ALIGNMENTS

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; STRANDEDNESS:
; TOPOLOGY: lin
; MOLECULE TYPE:
US-09-040-005-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-040-005-2
                                                                             Query Match
Best Local Similarity
Matches 218; Conser
                                                                                                                                                                                                                                                        TELEFAX: 617-876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENCTH: 538 antho acids
TYPE: antho acid
                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GIS3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-498-8224
TELEPHONE: 617-698-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 CmabridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Donaldson, Debra
APPLICANT: Unger, Michelle
TITLE OF INVENTION: MU-1 RE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: b, Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
ZIP: 02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
20 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/040,005
                   1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
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                                                                             Conservative
                                                                                                                                                                                                                        linear
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                                                                           100.0%; Score 1195; DB 3; 100.0%; Pred. No. 7.1e-123; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Debra
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                                                                             Indels
                                                                                                                Length 538;
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Gaps

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APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Holly, Richard D.
APPLICANT: Holson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Billon, Stacey R.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAII LIGAND
FILE REFERENCE: 99-16
                                                                                             RESULT 3
US-09-522-217-97
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US-09-522-217-115
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SOFTWARE: FASTSEQ for W
SEQ ID NO 115
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
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      GENERAL INFORMATION:
                                Sequence 97, Application Patent No. 6307024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER APPLICATION NUMBER: US 60/142,013
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                                                                                                                                                                                                                                                                                                                                                                                              SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
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                                                                                                                                                                                                                                                                                                                                     SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRKLISVDSRSVSLLPLEFRKDSSYELQ 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 1195; DB 4; 100.0%; Pred. No. 7.1e-123;
                                                             US/09522217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Andrew J.
APPLICANT: Nelson, Angela K.
APPLICANT: Hammond, Angela K.
TITLE OF INVENTION: NOVEL CYTOKINE ZALPHAll LIG
FILE REFERENCE: 99-16
FILE REFERENCE: 99-16
CURRENT APPLICATION NUMBER: US/09/522,217
CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER FILING DATE: 1999-03-11
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-07-01
SEQ ID NO 97
LENGTH: 606
myder: Dept
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US-08-599-455B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/08599455B Patent No. 5972621
GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: No. 6307024ak, Jul
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Specification of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                    APPLICANT: Culpepper, Janice A. TITLE OF INVENTION: METHODS OF IDETITLE OF INVENTION: MODULATE BODY NUMBER OF SEQUENCES: 44
                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
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                                                                                                                                                STREET: 225 F
CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                      COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                             ADDRESSEE: Fish & Richardson, STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 6307024ak, Julia
                                                                                                                                                                                                                                                                                        Tartaglia, Local Tepper, Robert I.
Tepper, Robert I.
Culpepper, Janice A.
Culpepper, Janice A.
METHODS OF IDENTIFYING COMPOUNDS THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1195; DB 4;
Pred. No. 8.5e-123;
); Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [F]
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RESULT 5
US-09-069-781B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569,485
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 07-00V-1995
APPLICATION NUMBER: 08/562,663
FILING DATE: 27-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Meild-john, Ph. D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/0170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 894 amino acids
                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                   TITLE OF INVENTION: THE OB RECEPTOR AND METHODS FOR TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF BODY WEIGHT DISORDERS, TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS: ADDRESSE: Fish & Richardson, P.C. STREET: 225 Franklin Street
                                                                                                                                                                                        APPLICANT: Tartaglia, Louis A. APPLICANT: Tepper, Robert I. APPLICANT: Culpepper, Janice A. APPLICANT: White, David W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 22-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH----FMADDIFSVNITDQSGNYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 28-DEC APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX:
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FastSEQ for Windows Version
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28-DEC-1995
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RESULT 6
US-08-618-957A-12
Sequence 12, Application US/08618957A
Patent No. 6355237
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APPLICATION NUMBER: US 08/599,455
FILING DATE: 22-TAN-1996
APPLICATION NUMBER: US 08/583,153
FILING DATE: 28-DEC-1995
APPLICATION NUMBER: US 08/570,142
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: US 08/569,485
FILING DATE: 08-DEC-1995
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: US 08/566,622
FILING DATE: 04-DEC-1995
APPLICATION NUMBER: US 08/562,663
APPLICATION NUMBER: US 08/562,663
APPLICATION NUMBER: US 08/562,663
APPLICATION TIPORMATION:
APPLICATION TIPORMATION:
ANAME: Maikleichn. Ph.D., Anita L.
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
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ZIP: 02110-2:
COMPUTER READAB:
MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/864,564
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/708,123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                        327 TTQ 329
                                                                                                                                                                                                                                                                                                                        146 DPWAVSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF 204
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                                                                                                                                                                                                                                                                                                                                                                            228 LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYLENS
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APPLICATION NUMBER: US 08
APPLICATION NUMBER: US 08
APPLICATION OF 05 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYS 87
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                                                                                                                                                                                                                                                                                                                                                                                                                          QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKDSFQTVQCNCSLRGC------ECHVPVPRAKLNYALLMYLEITSAGVSFQSPLMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s: 894 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
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RESULT 7
US-08-599-455B-43
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 894 amino acids
TYPE: amino acid
                                   Sequence 43, Application US/08599455B Patent No. 5972621 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICALLE.

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: POISSANT, Brian M.

REGISTRATION NUMBER: 28,462

REFERENCE/DOCKET NUMBER: 0089

TELECOMMUNICATION INFORMATION:

"""".FPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618,9:
FILING DATE: 20-MAR-1996
CLASSIETCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 10036-2811
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zupancic, Thomas Joel
APPLICANT: Shafer, Alan Wayne
TITLE OF INVENTION: METHODS FOR USING THE OBESE
TITLE OF INVENTION: GENE AND ITS GENE PRODUCT TO STIMULATE HEMATOPOIETIC
TITLE OF INVENTION: DEVELOPMENT
NUMBER OF SEQUENCES: 28
    APPLICANT:
                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                           327 TTQ 329
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                                                                                                                                                                                                                                                                                       146 DPWAVSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF 204
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                                                                                                                                                                                                                                                                                                                                                                88 QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                       39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FWADDIFSVNITDQSGNYS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
mes 57; Conserv
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TOPOLOGY: 11r
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Pennie & Edmonds LLP
1155 Avenue of The Americas
Tartaglia, Louis A.
Tepper, Robert I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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c, Thomas Joel
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US-09-069-781B-43; Sequence 43, Application US/09069781B; Patent No. 6287782
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; FRAGMENT TYPE:
US-08-599-455B-43
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.1%; Score 144; DB 2; Best Local Similarity 31.1%; Pred. No. 6.5e-07; Matches 57; Conservative 22; Mismatches 60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/583,153
FILING DATE: 28-DEC-1995
FILING DATE: 08/570,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,283
REFERICE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/570
FILING DATE: 11-DEC-1995
APPLICATION NUMBER: 08/569
FILING DATE: 08-DEC-1995
APPLICATION NUMBER: 08/566
FILING DATE: 04-DEC-1995
FILING DATE: 04-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS THAT
TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                             205 QTQ 207
                                                                                                                                                                                                                           146 DPWAYSPRRKLISYDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: v. TELEFAX: v. 200154
                                                                                                                        327 TTQ 329
                                                                                                                                                                                                      277 T--IVREAAEIVSATSLLVDSVLP-----GSSYEVQVRSKRLDGS---GVWSDWSSPQVF 326
                                                                                                                                                                                                                                                                                 228 LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYLENS 276
                                                                                                                                                                                                                                                                                                                                                             177 LKDSFQTVQCNCSLRGC-----ECHVPVPRAKLNYALLMYLEITSAGVSFQSPLMS 227
                                                                                                                                                                                                                                                                                                                                                                                             39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYS 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: ot. - 8906
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ZIP: 02110-2804
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STATE: MA
                                                                                                                                                                                                                                                                                                                    88 QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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STREET: 225 Franklin Street
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for Windows Version 2.0
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 29-APRIL-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/86
FILING DATE: 28-MAY-1997
APPLICATION NUMBER: US 08/70
FILING DATE: 03-SEP-1996
                                                                                                                                                                                                                                                    MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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APPLICANT: White, David W.
TITLE OF INVENTION: THE DB RECEPTOR AND METHODS FOR
TITLE OF INVENTION: THE DIAGNOSIS AND TREATMENT OF
TITLE OF INVENTION: INCLUDING OBESITY AND CACHEXIA
                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 07334/082001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
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ATTORNEY/AGENT INFORMATION:
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228 LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYLENS 276
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                                    88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/566,622 FILING DATE: 04-DEC-1995 APPLICATION NUMBER: US 08/562,663
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APPLICATION NUMBER:
FILING DATE: 28-DE
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                                                                                                         39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYS 87
                                                                                                                                                                                                                                                                                         TOPOLOGY:
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FILING DATE: 08-DEC-1995
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                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                          CENGTH:
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                                QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG 145
                                                                     LKDSFQTVQCNCSLRGC-----ECHVPVPRAKLNYALLMYLEITSAGVSFQSPLMS
                                                                                                                                              57;
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                                                                                                                                              Conservative
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28-мау-1997
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22-JAN-1996
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                                                                                                                                            22;
                                                                                                                                                            Score 144; DB 4; Length 1162; Pred. No. 6.5e-07;
                                                                                                                                              Mismatches
                                                                                                                                              60;
                                                                                                                                            Indels 44;
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US-08-640-389A-12
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Best Local :
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 12:
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APPLICANT:
APPLICANT:
APPLICANT:
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MEDJIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: unknown MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 896 amino acid
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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NAME: Poissant, Brian M.
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                                                                                                                                                                                      128 DIECWMKGDLKTFICHMEPLPKNPFKNYDSKVHLLYDLPEVIDDSPLPPLKDSFQTVQCN 187
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157 ISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQ 207
                                                                                                            188 CSL-----RGCXECHVPVPRAKLNYALLMYLEITSAGVSFQSPLMSLQ--PMLV--- 234
                                  235 VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYL-ENSTIVREAAXEI 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 89
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                                                                        99 IKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKL 156
                                                                                                                                                46 CSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYSQECGSFLLAES 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE:
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Similarity 28.4%; Pred. No. 6.5e-07
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(212) 869-9741/8864
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                                                                                                                                                                                                                                                              Conservative
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of the Americas
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RESULT 11
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FILING DATE: 05-MAR-1990
:SEQ ID NO:4:
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;Pateent No. 5198359
;APPLICANT: TANIGUCHI, TADATSUGU;JATAKEYAMA, MASANORI;
;MINAMOTO, SEJIRO;KONO, TAKESHI;DOI, TAKESHI;MIYASAKA, MASAYUKI;
;MINAMOTO, MITTSITRI:KARASUYMA, HAJIME
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;SEJIRO;KONO, TAKESHI;DOI, TAKESHI;MIYASAKA, MASAYUKI;TSUDO,
;MITSURU;KARASUYAMA, HAJIME
                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                            Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 865,155
FILING DATE: 08-APR-1992
APPLICATION NUMBER: 487,059
FILING DATE: 05-MAR-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2 NUMBER OF SEQUENCES: 12 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: RECOMBINANT PROTEIN RECEPTOR FOR IL-2
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 SYLSLKQRQQWLFLEMLIPSTSYEVQVRVKAQRNNT--GTWSPWSQPLTFRTRPADPMKE 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         155 KLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQ-SEELKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 LVAPHSLQVLHIDTQRCNISWKVSQVSHYIEP-----YLEFEARRRLLGHSWEDA---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : | | | |:||
288 VSATSLLVDSVLP--
73 TCELTLVRQASWACNLILGSFPESQSLTSVDLLDINVVCWEEKGWRRVKTCDFHPFDNLR 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCHMDVFH------FMADDIFSVNIT--DQSGNYSQECGSFLLAESIK 100
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                                                                                                                                                                                                                                                                                LENGTH: 539
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US, FILING DATE: 9-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 539
                                                                                                               1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
                                                                         CSHLECFYNSRANVSC---MWS-HEEALNV-----TICHVHAKS-NLRHWNK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCELTLYRQASWACNLILGSFPESQSLTSYDLLDINVVCWEEKGWRRYKTCDFHPFDNLR 132
                                                                                                                                                            Conservative
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                                                                                                                                                                            11.8%; Score 141.5; DE 22.5%; Pred. No. 4e-07;
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                                     -----FMADDIFSVNIT--DQSGNYSQECGSFLLAESIK 100
                                                                                                                                                       43;
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                                                                                                                                                            Mismatches
                                                                                                                                                                                             DB 6;
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Best Local
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILLING DATE: 19-CCT-1990
ATTORNEY/AGENT INFORMATION:
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PATE: PatentIn Release #1.0, Version #1.25

OURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/078.311

FILING DATE: 18-JIM-17.
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APPLICANT: Vigon, Isabelle
APPLICANT: Wigon, Isabelle
APPLICANT: Wendling, Francoise
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
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330 IWENCEEEEKTNPGLQTPQFSRCHFKSRNDSIIHIL-----VEVTTAPGTVHSYLGSPF 383
                                                                                 289
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                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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REFERENCE/DOCKET NUMBER: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Kowalchyk, Katherine M. REGISTRATION NUMBER: 36,848
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CITY: Minneapolis
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                                                                                                                       4 LYCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSL--HRSAHNATHATY- 60
                                                                               LQCFTLDLKNVTC---
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                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                          peptide
                                                                                                                                                                                  11.6%;
                                     ---TCHM-----DVFHFMADDIFSVNITDQSGNYSQECGS-F 93
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                                                                               ----QWQQQ-----DHASSQGFFYHSRARCCPRDRYP 329
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                                                                                                                                                                                  Score 139; DB 2;
Pred. No. 6.6e-07;
                                                                                                                                                                 Mismatches
                                                                                                                                                                   76;
                                                                                                                                                                                                      Length 493
                                                                                                                                                                 Indels 86;
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US-08-460-402-7
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                                                                                  TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                         TELEPHONE: 612-332-5300
                                                                                                                                                                                                                                 FILING DATE: 14-OCT-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 14-OCT-1990
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APPLICATION NUMBER: I
FILING DATE: 18-JUN-
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               MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 08/309,259 FILING DATE: 20-SEP-1994 CLASSIFICATION: 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94 LLAESIK-PAPPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG-DPWAVS 151
                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 436
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                                  TOPOLOGY:
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                                                                                                                                                                                                 REGISTRATION NUMBER:
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                                                                                                                                                                                                                    Randall A. Hillson
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Penciolelli, Jean-Francios
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RESULT 14
US-08-184-327A-4
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Best Local Similarity
Matches 59; Conserv
                                                                                                                             Matches
                                                                                                                                                            Query Match
                                                                                                                                            Best Local
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                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Nichol, Janet L.
TITLE OF INVENTION: Compositions And Methods For Stimulating
TITLE OF INVENTION: Platelet Production
                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                    TOPOLOGY: li
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                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 91320-1789
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                                                       LQCFTLDLKNVTC------QWQQQ-----DHASSQGFFYHSRARCCPRDRYP 329
                                                                                                                                            Similarity
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Hunt, Pamela
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                                                                                                                                                                                                                                      protein
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                                                                                                                         11.6%; Score 139; DB 1; Length 635; 24.0%; Pred. No. 9.5e-07; tive 25; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.6%; Score 139; DB 2; 24.0%; Pred. No. 6.6e-07; 24.0% 25; Mismatches 76;
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-TCHM-----DVFHFMADDIFSVNITDQSGNYSQECGS-F 93
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US-08-078-311-1
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/078,311
FILING DATE: 18-JUN-1993
CLASSIFICATION 1435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR90/00762
FILING DATE: 19-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: KOWALCHYK, Katherine M.
REGISTRATION NUMBER: 36,848
PREDINGENCYPER SUNDERS. 3676 BATTCHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08078311 Patent No. 5925750
                                                         Query Match 11.6%; Score 139; DB 2; Length 635, Best Local Similarity 24.0%; Pred. No. 9.5e-07; Matches 59; Conservative 25; Mismatches 76; Indels
                                                                                                                                                                                                                                                                                      TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 635 amino acids
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REFERENCE/POCKET NUMBER: 807
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Merchant & Gould
STREET: 3100 No. 5925750west Center
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT: Vigon, Isabelle
APPLICANT: Wendling, Francoise
TITLE OF INVENTION: Polypeptide of a Growth Factor Receptor
TITLE OF INVENTION: Family, Application in the Diagnosis and Treatment of
TITLE OF INVENTION: Myeloproliferative Disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 3100 ...
CITY: Minneapolis
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4 LVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSL--HRSAHNATHATY- 60
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Penciolelli, Jean-Francios
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                                                                PRRKLISVDSRSVSLLP------LEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVI 203
                                                                                                                                        IWENCEEEKTNPGLQTPQFSRCHFKSRNDSIIHIL----
                                                                                                                                                              -----DVFHFMADDIFSVNITDQSGNYSQECGS-F
488
                                            -LEPPLGARGGTLELRPRSRYRLQLRA-RLNGPTYQGPWSSWSDPTR 482
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Search completed: June 28, 2002, 07:41:41 Job time: 56 sec

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Title:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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MEDLINE-90319131, PubMed=1695379;

MEDLINE-90319131, Toh N., Kitamura T., Schreurs J., Yonehara S.,

A Gorman D.M., Itoh N., Kitamura T.,

Yahara I., Arai K., Miyajima A.;

"Cloning and expression of a gene encoding an interleukin 3 recept

"Ithe protein: identification of another member of the cytokine

receptor gene family.",

Proc. Natl. Acad. Sci. U.S. AB7:5459-5463(1990).

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --SSLHTSNFQVNLEPKLFLPNSIYAARVRTRLSAGSSLSGRPSRWSPEVHWDSQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAQHVQPPPPKDIHISPSGDHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRLQDSWEDA-
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878
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                                                                  Csf2rb1.
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Rodentia;
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OF N-LINKED (GLCNAC. . .) (PO N-LINKED (GLCNAC. . .) (PO N-LINKED (GLCNAC. . .) (PO N-LINKED (GLCNAC. . .))
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         145;
No. 3.
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.2e-05;
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                                                                                                                                                                                                                                                                                                                                                                                                                         THE BETA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 49; Conser
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DISULFID
CARBOHYD
CARBOHYD
CARBOHYD
SEQUENCE
  STRAIN-C57BL/KSJ; TISSUE-Hypothalamus; MEDLINE-96190816; PubMed-8608603; Chen H., Charlat O., Tartaglia L.A., Woolf E.A., Weng X., Ellis S.J., Lakey N.D., Culpepper J., Moore K.J., Breitbart R Duyk G.M., Tepper R.I., Morgenstern J.P.; Tepper R.I., Morgenstern J.P.; dentification of a mutation in the leptin receptor gene in diabetes.
                                                                                                                                                                                                    Tartaglia L.A., Dembski M., Weng X., Deng N., Culper Devos R., Richards G.J., Campfield L.A., Clark F.T., Muir C., Sanker S., Moriarty A., Moore K.J., Smutko Mays G.G., Woolf E.A., Monroe C.A., Tepper R.I.; "Identification and expression cloning of a leptin r Cell 83:1263-1271(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEPR_MOUSE STANDARD: PRT; 1162 AA. P48356; 035686; 061215; Q64309; 054986; 01-FEB-1996 (Rel. 33, Created) 01-FEB-1996 (Rel. 33, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Leptin receptor precursor (LEP-R) (OB receptor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                     TISSUE=Choroid plexus;
MEDLINE=96128129; PubMed=8548812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003531; Hematopo_receptor_S_F1
Pfam; PF00041; fn3; 2.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (VARIANT A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor).
LEPR OR OBR OR DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 DLVCYTDYLQTVICILEMWN------LHPSTLTLTWQDQYEELKDEATSCSLHRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QLEPDTSYCARVKPI--SNYDGIWSKWSEEYTWKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-RDSYSLHWETQKMAYSFI----EHTFQVQYKKKSDSWEDSKTENLDRAHSMDLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGASVYTRYHCSLPVPEPSAHSQYTVSVK-----HLEQGKFIMSYNHIQMEPPTLNLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLA-ESIKPAPP-FNVTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NLQCFFDGIQSLHCSWEVWTQTTGSVSFGLFYRPSPVA-----PEEKCSPVVKEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQT
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442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Mouse).
etazoa; Chordata;
theria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22
896
441
463
896
241
440
440
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9111
                                                                                                                                                           (VARIANT B)
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CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (P

N-LINKED (GLCNAC. . . ) (P

N-LINKED (GLCNAC. . . ) (P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 144; DB 1
Pred. No. 4e-05;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
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CYTOKINE RECEPTOR COMMON BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Sciurognathi; Muridae;
                                                                                                                                                                                                                              cloning of a leptin receptor, OB-R.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8CE16EDFDC07A999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439
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                                                                                                                                                                                                                                                                         rk F.T., Deeds Smutko J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal
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(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
; Murinae; Mus
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         db/db
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RL GENOMICS 45:264-270(1997).

CC -!- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

CI -!- FUNCTION: THE SHORT FORM (VARIANT A) MAY ACT TO TRANSPORT LEPTIN

TO THE CEREBROSSINAL FLUID. THE PUTATIVE SOLUBLE RECEPTOR (VARIANT E) COULD FUNCTION AS A TRANSPORT PROTEIN.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXCEPT FOR FORM E

CC WHICH COULD BE SECRETED.

CC HAITERNATIVE PRODUCTS: 5 ISOFORMS; A, B (SHOWN HERE), C, D AND E;

CC ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: (1) VARIANT A: HIGHEST LEVEL OF EXPRESSION IN

CC LUNG AND KIDNEY, ALSO PRESENT IN CHOROID PLEXUS AND HYPOTHALAMUS.

CC (2) VARIANT B: HIGHEST LEVEL OF EXPRESSION IN HYPOTHALAMUS AND

CC LOWER LEVEL IN BRAIN, TESTES AND ADIPOSE TISSUE. (3) VARIANT E:

CC EXPRESSED IN ADIPOSE TISSUE, HYPOTHALAMUS, HEART, AND TESTES.

CC -: SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mice.
Cell
[3]
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STRAIN-NEW ZEALAND OBESE / NZO; TISSUE-Hypothalamus;
MEDLINE-97462708; PubMed-9322935;
Igel M., Becker W., Herberg L., Joost H.G.;
"Hyperleptinemia, leptin resistance, and polymorphic in the New Zealand obese mouse.";
Endocrinology 138:4234-4239(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cloffi J.A., Shafer A.W., Zupancic Mikhail A., Platika D., Snodgrass "Novel B219/OB receptor isoforms: hematopoiesis and reproduction."; Nat. Med. 2:585-589(1996).
                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by are entitles requires a license content.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chung W.K., Leibel R.L.; Hund H., Error Frine structure of the murine leptin suppression is required to form two a transcripts.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=FVB/N; TISSUE=Spleen;
MEDLINE=96270520; PubMed=8692797;
Ghilardi N., Ziegler S., Wiestner A., Stoffel R., Heim M.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cioffi J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (VARIANT C).
STRAIN-BALB/C; TISSUE-Liver;
MEDLINE-96206286; PubMed-8616721;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lee G.-H., Proenca R., Montez J.m., Callul N.W., Collins J.M.;
Lee J.I., Friedman J.M.;
"Abnormal splicing of the leptin receptor in diabetic mice.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (VARIANTS A TO E). STRAIN=C57BL/KS; TISSUE=Hypothalamus; MEDLINE=96231997; PubMed=8628397;
                                                                                                                                                                                                  This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98008913; PubMed=9344648; Chua S.C., Koutras I.K., Han L., Liu
EMBL; U42467; AAA93014.1;
EMBL; U46135; AAC52408.1;
EMBL; U49106; AAC52420.1;
EMBL; U49107; AAC52421.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Skoda R.C.;
"Defective
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                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                  between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STAT signaling by the leptin receptor in diabetic mice.", Acad. Sci. U.S.A. 93:6231-6235(1996).
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nodgrass H.R.;
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                                                                                                         (See http://www.isb-sib.ch/announce/
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InterPro; IPR003961; FN_III.
InterPro; IPR003399; Hematopo_receptor_L_F2.
Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 3.
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U49109; AAC5244.1;
U49110; AAC5244.1;
U59115; AAC52599.1;
U52915; CAA71343.1;
U508661; AAC52705.1;
U50863; AAC52707.1;
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AF039453; AAB95334
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Receptor; Transmembrane; Glycoprotein;
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V -> I (IN STRAIN NOZ).
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A -> T (IN REF. 5).
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01-AUG-1990
01-AUG-1990
01-FEB-1995
                                                                                                                                                                                                                                                                                                                                    expression in lymphoma line EL-4 caused by a promoter insertion.";
proc. Natl. Acad. Sci. U.S.A. 87:1806-1810(1990).
-I- FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
MITOGENIC SIGNALS OF IL-2.
-I- SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
                                                                                                            MGD;
                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                      InterPro; IPR003531; H
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kono T., Doi T., Yamada G., Hatakeyama M., Minamoto S., Miyasaka M., Miyata T., Taniguchi T.; Murine interleukin 2 receptor beta chain: dysregulated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-AUG-1990 (Rel. 15, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
Interleukhn-2 receptor beta chain precursor (IL-2 I
(High affinity IL-2 receptor beta subunit) (CD122).
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Receptor;
                                                                                                                          HSSP;
                                                                                                                                                     EMBL; M28052; AAA39283.1;
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                                                                                                                                                                                                  entities
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                        PROSITE; PS01355;
                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                            WITH A GAMMA CHAIN.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                        A35052; A35052.
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MGI:96550; Il2
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57; Conser
                                                                                                                                                                                 an email to license@isb-sib.ch).
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                                                          IPRO02996; CRIA.
IPRO03961; FN_III.
IPRO03531; Hematopo_receptor_S_F1
                                                                                                                                                                                                  requires
            Transmembrane;
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                        HEMATOPO_REC_S_F1;
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Rodentia;
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          Glycoprotein;
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Pred.
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No. 5
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ALD DESCRIPTION OF THE PROPERTY OF THE PROPERT
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TPOR_HUMAN
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Best Local
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P40238;
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01-FEB-1995
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CHAIN
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                                                                                                                                                                                                                                                                                                                                           WEDLINE=92302297; PubMed=1608974;
Vigon I., Mornon J.-P., Cocault L., Mitjavila M. Gisselbrecht S., Souyri M.;
"Molecular cloning and characterization of MPL, "Molecular cloning and characterization of a member o growth factor receptor superfamily.";
Proc. Natl. Acad. Sci. U.S.A. 89:5640-5644(1992)
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                                                                                                                                                                                                                Chretien
                                                                                                                                                                                                                                    Mignotte V.,
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=94292186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54;
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nilarity 22.5%;
Conservative 4:
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation updat
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EXTRACELLULAR (POTENTIAL).
POTENTIAL.

POTENTIAL.

CYTODLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

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N-LINKED (GLCNAC. . .) (POTENINGLINKED (GLCNAC. 
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EMBL; U681...

R EMBL; U68160; ...
DR EMBL; U68161; AAB...
PIR; A45266; A45266.
"SSP; P19235; 1EBA.
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
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                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
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SMART; SM00060; FN3; 2
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1
                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS01352; HEMATOPO_REC_L_F1;
                                                                  289
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DISEASE: DEFECTS IN MFL ARE A CAUSE OF CONGENITAL AMEGAKA THROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED BY ISOLATHROMBOCYTOPENIA AND MEGAKARYOCYTOPENIA WITH NO PHYSICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CAUTION: IT IS UNCERTAIN WHETHER MET 1 OR MET-8 IS THE IN
DATABASE: NAME-PROW; NOTE-CD guide CD110 entry;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; M90102; AAA69971.1; -..., M90103; AAA69972.1; -...; U68162; AAB08424.1; JOIN U68159; AAB08424.1; JOIN U68161; AAB08424.1; AAB08424.1; AAB08424; AAB08424.1; AAB08424; AAB08424; AAB08424; AAB08424; AAB08424; AAB08424; AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/l1586825_g.htm".
                                                                  LQCFTLDLKNVTC--
                                                                                                            LYCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSL-~HRSAHNATHATY~
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ARE ALWAYS FOUND TO BE COEXPRESSED.
SEASE: DEFECTS IN MPL ARE A CAUSE OF CONGENITAL AMEGAKARYOCYTIC
ROMBOCYTOPENIA (CAMT); A DISEASE CHARACTERIZED BY ISOLATED
                                                                                                                                                                               Similarity
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JOINED.
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TCHM-----DVFHFMADDIFSVNITDQSGNYSQECGS-F 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                            Score 139; DB 1;
Pred. No. 7.3e-05;
                                                                                                                                                                                                                                                                                                                                     MISSING (IN ISOFORM C-MPL-P)
A -> V (IN DBSNP:6087).
/FTId=VAR_011988.
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                                                                                                                                                                                                                                                                   E -> K (IN DBSNP:6088).
/FTId=VAR_011989.
D25D8D8959359DDC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLRHALWPSLPDLHRVLGQYLRDTAALSPPKATVSDTCEEV EPSLLEILPKSSERTP -> YRPRQAGDWRWTRWSRTCKQA
                                                                                                                                                                                                                                                                                                                                                                                                                                   FLVRSVTPDLRPPPVRTYGFALPARHLWDSPRLLTL (IN
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                                                                --- QQQQWQ---
                                                                                                                                                           Mismatches
                                                                  -- DHASSQGFFYHSRARCCPRDRYP
                                                                                                                                                                                                  Length 635
                                                                                                                                                           Indels
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STANDARD; P70494; P70495; Q63985;
Q62959; Q63007; P70493; P70494; P70495; Q63885;
P97889; Q35772;
15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
Q1-MAR-2002 (Rel. 41, Last annotation update)
Leptin receptor precursor (LEP-R) (OB receptor)
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STRAIN-ZUCKER; TISSUE-Hypothalamus;
MEDLINE-96241565; PubMed-8673096;
                                                                                      "Phenotype-linked amino acid alteration in leptin receptor cDNA frozucker fatty (fa/fa) rat.";
Biochem. Biochem.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (VARIANT B).

Karlsson C., Lindell K., Robinson I.C.A.F., Carlsson L.!

Carlsson B.;

"Cloning of the rat leptin receptor.";

"Cloning of the rat leptin receptor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LEPR OR OBR OR FA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takaya K., Ogawa Y., Isse N., Okazaki T., Satoh N., Masuzaki H. Mori K., Tamura N., Hosoda K., Nakao K.;
"Molecular cloning of rat leptin receptor isoform complementary DNAs -- identification of a missense mutation in Zucker fatty (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tida M., Murakami T., Ishida K., Mizuno A., Kuwajima M., "Substitution at codon 269 (glitamine --> proline) of the receptor (OB-R) cDNA is the only mutation found in the Zi (fa/fa) rat.";
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Mammalia; E
SEQUENCE OF 1-123 FROM N.A.
Morishita T., Hidaka T., Ku
                                                                                                                                                 Iida M., Murakami T., Ishida K
                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND VARIANT FA PRO-269 (VARIANT A).
STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochem. Biophys. Res. Commun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-SPRAGUE-DAWLEY, AND ZUCKER FATTY; MEDLINE-96332408; PubMed-8769097;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Biochem. Biophys. Res. Commun. 224:597-604(1996)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hess J.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Leptin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q., Hammond H.A.,
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Kuzuyama
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T., Noguchi T.;
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Q63385; Q63386; Q54805;
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TISSUE=Brain;
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the leptin
Zucker fatty
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RT RAPRAMENTAL RAPRAMENTA R
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EMBL: D84550; BAA12697.1; ...
EMBL: D84551; BAA12698.1; ...
EMBL: D85557; BAA12830.1; ...
EMBL: D85558; BAA12831.1; ...
EMBL: D85559; BAA12832.1; ...
EMBL: D85559; BAA12832.1; ...
EMBL: D85559; BAA12832.1; ...
EMBL: D84125; BAA12230.1; ...
EMBL: D84125; BAA12230.1; ...
EMBL: D84126; BAA12231.1; ...
EMBL: D84126; BAA12231.1; ...
EMBL: D84126; BAA12231.1; ...
EMBL: D84126; BAA12231.1; ...
EMBL: D84126; BAA24899.1; ...
EMBL: AF001708.18; BAA24899.1; ...
EMBL: AF007818; AAB63201.1; ...
EMBL: AF007818; AAB63201.1; ...
InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_re
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Submitted
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Chua S.C. Jr., White D.W., Wu-Peng X.S., Liu S.M.,
Kershaw E.E., Chung W.K., Power-Kehoe L., Chua M.,
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                                                                                                                                                                                                                            PROSITE; PS01353; HEMATOPO_REC_L_F2; 1. Obesity; Receptor; Transmembrane; Glyco
                                                                                                                                                                                                                                                                                  Pfam; PF00041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Leibel R.L.; "Phenotype of fatty due to Gln269Pro mutation in the leptin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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the EMBL/GenBank/DDBJ databases
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LEPTIN RECEPTOR.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 3.

FIBRONECTIN TYPE-III 3.
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                                                                                                                                                                                                                       Glycoprotein;
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Tartaglia L.A.,
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TISSUE=Brain;
MEDLINE=96128129; PubMed=8548812;
Tartaglia L.A., Dembski M., Weng X., Deng N., Culpepper J.,
Tartaglia L.A., Campfield L.A., Clark F.T., Deeds
Devos R., Richards G.J., Campfield L.A., Clark F.T., Deeds
Muir C., Sanker S., Moriarty A., Moore K.J., Smutko J.S.,
                                                                                                                                            Leptin receptor precu
LEPR OR OBR.
Homo sapiens (Human).
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                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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(Rel. 33, Last sequence update)
(Rel. 41, Last annotation update)
ptor precursor (LEP-R) (OB receptor)
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Pred. No. 0.00019
3; Mismatches 6
                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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DRR CCCCCCCCCCCCCRETAR RANGE
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Diabetes 45:992-994(1996).
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MEDLINE-97431549; PubMed-9287054;
Chung W.K., Power-Rehoe L., Chua M., Chu F., Aronne L., Huma Z.,
Sothern M., Udall J.N., Kahle B., Leibel R.L.;
"Exonic and intronic sequence variation in the human leptin receptor
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gene (LEPR).";
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1- FUNCTION: RECEPTOR FOR OBESITY FACTOR (LEPTIN).

1- SIMILARITY: CONTAINS: Type I membrane protein.

1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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MEDLINE-962/0489; PubMed-8566155;
Considine R.V., Considine E.L., Wi
"The hypothalamic leptin receptor
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MEDLINE=99075638;
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MEDLINE=97289527;
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Biesterfeldt J
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                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=97318795; PubMed=9175732;
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U59248;
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AAA93015.1;
AAB09673.1;
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AAB09673.1;
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PubMed=9860295;
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Pfam; PF00041; fn3; 2.
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Obesity; Receptor; Transmembrane; G1
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  PPLGLHMEITDDGNLKISWSSP---
                                     PP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVD 160
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MW; 8FF21D9AF5125808 CRC64;
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Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon Fuhrmann J., Mason T., Crosby M.L., Barnstead M., Cronin Deslattes Mays A., Cao Y., Xu R.Y., Kang H.-L., Mitchell Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;
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Genomics 60:295-308(1999).
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Int. Immuno
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MEDLINE=90171849; PubMed=2307934;
Idzerda R.L., March C.J., Mosley B., Lyman S.D., Bos T.V.,
Gimpel S.D., Din W.S., Grabstein K.H., Widmer M.B., Park L.S.,
Cosman D., Beckmann M.P.;
"Human interleukin 4 receptor confers biological responsiveness
defines a novel receptor superfamily.";
J. Exp. Med. 171:861-873(1990).
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VARIANTS VAL-75; ALA-400; ARG-431; LEU-436 AND PRO-786.
VARIANE-97224413; PubMed-9070874;
DeiChmann K., Bardutzky J., Forster J., Heinzmann A., Kuehr J.;
"Common polymorphisms in the coding part of the IL4-receptor ge
                                                                          Mitsuyasu H., Izuhara K., Mao X.-Q., Gao P.S., Arinobu Y., Enomo
Kawai M., Sasaki S., Dake Y., Hamasaki N., Shirakawa T., Hopkin
"Ile50Val variant of Ir4R alpha upregulates IgE synthesis and
associates with atopic asthma.";
Nat. Genet. 19:119-120(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-91120547.
MEDLINE-91120547.
Gallzzi J.-P., Zuber C.E., Harada N., Gorman D.M., Djossou O.,
Gallzzi J.-P., Zuber C.E., Harada N., Myajima A.;
Kastelein R., Banchereau J., Howard M., Myajima A.;
"Molecular cloning of a cDNA encoding the human interleukin 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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IL4R OR IL4RA OR 582J2.1.
VARIANT ATOPIC AS' MEDLINE=99322293;
                                                                                                                                                                                                                                                                                                                                                                              VARIANT ATOPIC ARG-576.
MEDLINE=98041803; pubMed=939269.
Hershey G.K.K., Friedrich M.F.,
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MEDLINE-98282087;
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Engl. J. Med.
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                                                                                                                                                                                                                                                                                                         of atopy with a the interleukin
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21, Last sequence up
41, Last annotation
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PubMed-10390422
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Primates;
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-4 receptor.":
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IPR002996; IPR003961;

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MEDLINE-21182661; PubMed-11285129;
AL LOZANO F., PLACES L., VILA J.M., Padilla O., Arman M., Gimferrer I.,
AL Suarzez B., Lopez de la Iglesia A., Miserachs N., Vives J.;
AL Suarzez B., Lopez de la Iglesia A., Miserachs N., Vives J.;
AL Tissue Antigens 57:216-220 (2001).
Tand definition of eight common alleles for human IL4RA exon 11.";
AL Tissue Antigens 57:216-220 (2001).
Tissue Tissue Tissue Tanguage Tanguage
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Ober C., Leavitt S.A., Tsalenko A., Howard T.D., Hoki D.M., Danie Newman D.L., Wu X., Parry R., Lester L.A., Solway J., Blumenthal King R.A., Xu J., Meyers D.A., Bleecker E.R., Cox N.J.;
"Variation in the interleukin 4-receptor alpha gene confers susceptibility to asthma and atopy in ethnically diverse populations.";
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Oiso N., Fukai K., Ishii M.;
"Interleukin 4 receptor alpha chain polymorphism Gln551Arg
associated with adult atopic dermatitis in Japan.";
Br. J. Dermatol. 142:1003-1006(2000).
                                                                                                                       EMBL;
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                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce or send an email to license@isb-sib.ch).
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Deichmann K.A.;
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Kobayashi K., Imoto N., Nakahara S., Matsui A., Hamaguchi
"No association between atopy/asthma and the Ile50Val pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                consequences.";
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Am. J. Respir. Crit. Care Med. 160:342-345(1999)
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TILZB_RAT STANDARD; PRT; 537 AA.

P26896;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-FBB-1996 (Rel. 33, Last annotation update)
Interleukin-2 receptor beta chain precursor (II-2 receptor) (P70-75)
(High affinity II-2 receptor beta subunit) (CD122).

Rattus norvegicus (Rat).
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PROSITE; PS01355; HEMATO,
Receptor; Transmembrane;
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Pfam; PF00041; fn3; 1.
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mbrane; Glycoprotein; Signal; Disease mutation;
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N-LINKED (GLCNAC...) (POTENTIAL).
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E -> A (IN DBSNP:1805011).
/FTId=VAR_011657.
C -> R (IN DBSNP:1805012).
/FTId=VAR_011658.
S -> L (IN DBSNP:1805013).
/FTId=VAR_011659.
S -> P (IN DBSNP:1805015).
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Pred. No. 0.00
25; Mismatches
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S -> P (IN 1.8% OF THE POPULATION; DBSNP:1805014).
/FTIG-VAR 011663.
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S -> A (IN DBSNP
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V -> I.
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Q -> R (IN ATOPIC PATIENTS)
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RA PAGE TI., Deliman M.J.

RA Page TI., Deliman M.J.

RY "Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha

RY and beta chain genes: differentially regulated gene activity in

RY response to mitogenic stimulation.";

REUT. J. Immunol. 21:2133-2138(1991).

REUT. J. IECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS

INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE

INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE

C MITOGENIC SIGNALS OF IL-2.

C MITOGENIC SIGNALS OF IL-2.

C SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R

C SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R

C EXIST IN 3 DIFFERENT FORMS: A HIGH APPINITY DIMER, AM INTERMEDIATE

C FORTHLY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA

C AFFIRITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA

C CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE

C SUBCELLULAR LOCATION: Type I membrane protein.

C -!- SUBCELLULAR LOCATION: Type I membrane protein.
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Mammalia; Eutheria; )
NCBI_TaxID=10116;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SP
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M55050; AAA41429.1; -.
HSSP; P14784; 1IIN.
InterPro; IPR002961; FN_III.
InterPro; IPR003951; FN_III.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 1.
SMARR; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE=91364784; PubMed=1889461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SM00060; FN3;
E; PS01355; HE
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                   HEMATOPO_REC_S_F1; 1.
HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein;
POTENTIAL
POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

N-LINED (GLCNAC...) (PO'
                                                                                                                                                                                                                                                                                                                                         INTERLEUKIN-2 RECEPTOR BETA CHAIN. EXTRACELLULAR (POTENTIAL).
                                          (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEA---TSCSLHRSAH----
RRRLLDRSWEDASVESLKQRQQWIFLETLTPDTSYELQVRVIAQRGKT~-RTWSPWSQPM
                                                              IRLIAPHSLQVLHIETRRCNISWEVSQVSHYVNP----YLEFE--
                                                                                    IKPAPPENVTVTF--SGQYNISWR----SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSP
                                                                                                                                                                NAT-----HATYTCHM------DVFHFMADDIFSVNIT--DQSGNYSQECGSFLLAES
                                                                                                                                                                                                CSHLKCFYNSRANVSC---MWS-----PEEALNVTSCHIHAKSDMRHW
                               RRKLISVDSRSVSLLPLEFRK-------DSSYELQVRAGPMPGSSYQGTWSEWSDPV 202
                                                                                                                                 NKTCELTPVRQASWACNLILGPLPDSQSLTSVDLLSLSVVCWEEKGWRRVKTCTFHPFDN
                                                                                                                                                                                                                                                                ch 11.2%;
1 Similarity 23.1%;
58; Conservative 4
                                                                                                                                                                                                                                                                  41;
                                                                                                                                                                                                                                                                Score 134; DB
Pred. No. 0.00
41; Mismatches
                                                                                                                                                                                                                                                        DB
,.00016;
72;
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Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Rc
NCBI_TaxID=10090;
This SWIS
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the Europ
use by
modified
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P34902;
01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytokine receptor common gamma chain precursor (Gamma-C)
Cinterleukin-2 receptor gamma chain) (IL-2R gamma chain)
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                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96341745; PubMed-8750189; Chiu R.K., Droll A., Cooper D.L., Dougherty G.J.; Molecular mechanisms regulating the adhesion protein CD44.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDILINE-95104285; PubMed-7805729; MEDILINE-95104285; PubMed-7805729; Disanto J.P., Certain S., Wilson A., Macdonald Fischer A., de Saint Basile G.; "The murine interleukin-2 receptor gamma chain chromosomal localization and expression in the Eur. J. Immunol. 24:3014-3018(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-93391374; PubMed-8378320;
Cao X., Kozak C.A., Liu Y.J., Nguchi M., O'Connell E., Leonard W.J.;
"Characterization of cDNAs encoding the murine interleukin 2 receptor
(IL-2R) gamma chain: chromosomal mapping and tissue specificity of
IL-2R gamma chain expression.";
Proc. Natl. Acad. Sci. U.S.A. 90:8464-8468(1993).
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MEDLINE-93277575; PubMed-8503926;

KUMBAKI S., Kondo M., Takeshita T., Asao H., Nakamura M.,

"Cloning of the mouse interleukin 2 receptor gamma chain:
demonstration of functional differences between the mouse receptors.";
                                                                                                                                                                                                                                                                                                                                                                      the adhesion protein CD44.";
J. Neurooncol. 26:321-239(1995).
-i- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-9336619; PubMed-8359699; KObayashi N., Nakagawa S., Minami Y., Taniguchi T., Y (Cloning and sequencing of the cDNA encoding a mouse
                                                                                                                                                                                                                                                                                                             -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                       INTERLEDININS.

INTERLEDININS.

INTERLEDININS.

SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-
SUBUNIT: THE GAMMA CHAIN IS RECEPTORS.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130:303-304(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biophys. Res. Commun. 193:356-363(1993)
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       binding activity
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                                                                                                                                                                                                                                                                                                                                                                      A VARIETY OF
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TPOR_MOUSE
ID TPOR_MOUSE
AC Q08351;
DT 01-FEB-1995 (
DT 01-FEB-1995 (
DT 16-OCT-2001 (
DE Thrombopoieti
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Best Local S
Matches 56
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EMBL; U21795 AA
EMBL; U2048; AA
EMBL; L10048; AA
EMBL; S75843; AA
EMBL; S75844; AA
EMBL; S75845; AA
EMBL; S75846; AA
EMBL; S75850; AB
EMBL; S7
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SIGNAL
CHAIN
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   Thrombopoietin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 25.: 56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CQIQKEDIQLYQTFVVQLQDPQKPQRRAVQKLNLQNLVIPRAPENLTLSNLSESQL
                      (Rel. 31,
(Rel. 31,
(Rel. 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BAA02974 1

BAA64276 1

BAA0276 1

AAA32928 1

AAB32904 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  issemembrane: Glycoprotein; Signal.

BY SIMILARITY.

BY CYTOKINE RECEPTOR COMMON GAMMA CHAIN.

33 369 CYTOKINE RECEPTOR COMMON GAMMA CHAIN.

33 263 EXTRACELLULAR (POTENTIAL).

44 POTENTIAL.

55 369 CYTOPLASMIC (POTENTIAL).

56 PIBRONECTIN TYPE-III.

77 POTENTIAL.

11 71 N-LINKED (GLCNAC...) (POTENTIAL).

78 N-LINKED (GLCNAC...) (POTENTIAL).

40 84 N-LINKED (GLCNAC...) (POTENTIAL).

41 84 N-LINKED (GLCNAC...) (POTENTIAL).

42 84 N-LINKED (GLCNAC...) (POTENTIAL).

43 96 N-LINKED (GLCNAC...) (POTENTIAL).

44 84 N-LINKED (GLCNAC...) (POTENTIAL).

45 96 N-LINKED (GLCNAC...) (POTENTIAL).

46 96 N-LINKED (GLCNAC...) (POTENTIAL).

47 N-LINKED (GLCNAC...) (POTENTIAL).

48 N-LINKED (GLCNAC...) (POTENTIAL).

49 164 N-LINKED (GLCNAC...) (POTENTIAL).

40 164 N-LINKED (GLCNAC...) (POTENTIAL).
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precursor (TPO-R) (My
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Pred. No. 0.00
33; Mismatches
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nes 94;
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   (Myeloproliferative
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      leukemia
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MEDLINE=93327753; PubMed=8334987;

MEDLINE=93327753; PubMed=8334987;
                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                                                                                                                                           DOMAIN
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z22649; CAA80365.1; -.
EMBL; Z22657; CAA80372.1; -.
EMBL; X73677; CAA52031.1; -.
PIR; S35317; S35317.
HSSP; P19235; 1EBA.
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncogene 8:2607-2615(1993).
-!- FUNCTION: RECEPTOR FOR THROMBOPOIETIN, MAY REPRESENT A REGULATORY MOLECULE SPECIFIC FOR TPO-R-DEPENDENT IMMINE RESPONSES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=ICFW; TISSUE=Fetal liver;
MEDLINE=9339034; PubMed=8397366;
Vigon I., Florindo C., Fichelson S., Guenet J.-L., Mattei
Souyri M., Cosman D., Gisselbrecht S.;
"Characterization of the murine Mpl proto-oncogene, a memb
hematopoistic cytokine receptor family: molecular cloning,
chromosomal location and evidence for a function in cell c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Skoda R.C., Seldin D.C.,
Leder P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein) (C-mpl). MPL OR TPOR.
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InterPro; IPR003961; FN_III.
InterPro; IPR00328; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor;
                                              281
  62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              musculus (Mouse)
                                              LQCFTLDLKMVTC--
                                                                                       LVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATYT--
                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PS01352;
                                                                                                                                                                                                                                                   26
26
483
505
117
2
9
9
222
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                   Æ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HEMATOPO_REC_L_F1; 1.
                                                                                                                                                                                                                                                                         25
625
482
504
625
117
117
222
                                                                                                                                                                                                                                                   69817
                                                                                                                                                       11.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal; Repeat.
                                                                                                                                                                                                                                                      WW.
                                                                                                                                      25;
                                                                                                                                 Score 132.5;
Pred. No. 0.00
25; Mismatches
                                                                                                                                                                                                                                                                  POTENTIAL.
CYTOPLASMIC (POTENTIAL).
N-LINKED (GLCNAC. . .) (P
MISSING (IN REF. 2).
D -> V (IN REF. 2).
P -> PPRISPAGE (IN REF. 2).
                                           ----QWQQQ-----DRTSSQGFFR--HSRTRCCPTDR
CHM-----DVFHFMADDIFSVNITDQSGNYSQECGS- 92
                                                                                                                                                                                                                                                                                                                                                                                                             THROMBOPOIETIN RECEPTOR. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                 -> V (ÎN REF. 2).
-> PVRTSPAGE (ÎN REF. 2).
309CF6EAA3724549 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peichel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no rest
                                                                                                                                   5; DB 1;
0.00027;
hes 80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and the
                                                                                                                                                                                                                                                                                                                                         .) (POTENTIAL).
                                                                                                                                                                               Length 625;
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mattei M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Vogt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       growth.";
                                                                                                                                      75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                for
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                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in no way
                                              319
                                                                                       61
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RESULT 12

CYRG_BOVIN

ID CYRG_BOVIN

STANDARD; PRT; 379 AA.

AC Q95118;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Cytokine receptor common gamma chain precursor (Gamma-C)

DE (Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           В
                                                                                                                                                                                                                                                                                                   use by non-profit institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
           CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                                                               DISULFID
DISULFID
CARBOHYD
                                                                                                      TRANSMEM
DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                               INTERLEUKINS.

1. SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, II PROBABLY ALSO THE IL-13 RECEPTORS.

1. SUBCELLULAR LOCATION: Type I membrane protein.

1. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

1. SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma gene.",
DNA Cell Biol. 15:453-459(1996).
-i- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=96268473; PubMed=8672241;
Yoo J., Stone R.T., Solinas-Toldo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                                                                                                EMBL; U33748; AAB07812.1; -. HSSP; P31785; 1ILN.
                                                                                                                                                             CHAIN
                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                 Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL2RG
SEQUENCE
                                                                                                                                              DOMAIN
                                                                                                                                                                                       Receptor;
                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloning and chromosomal mapping
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                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -SPRRKLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FWIHQAVLLPTPSCHWREVSSGRLELEWQHQSSWAA----QETCYQLRYTGEGREDWKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILAESI-KPAPPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG-DPWAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DPTWEKCEEEEPRPGSQPALVSRCHFKSRNDSVIHIL-----VEVTTAQGAVHSYLGSP
                                                                                                                                                                                                    PS01355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                         IPR003961; FN_III.
IPR003531; Hematopo_receptor_S_F1.
                                                                                                                                                                                                                                                                     IPR002996; CR1A.
               270
291
158
158
109
109
166
166
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              379
269
269
290
379
379
256
256
172
172
106
166
 43037
                                                                                                                                                                                       Glycoprotein; Signal.
 WW;
N-LINKED (GLCNAC...
                                                                                POTENT LAL
                                                                                            POTENTIAL.
                                                                                                         CYTOPLASMIC FIBRONECTIN
                                                                                                                                    POTENTIAL.
                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                              CYTOKINE RECEPTOR COMMON GAMMA CHAIN
                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ., Fries R., Beattie C.W.; bovine interleukin-2 receptor
            (GLCNAC...
(GLCNAC...
(GLCNAC...
(GLCNAC...
(GLCNAC...
                                                                                                         (POTENTIAL).
TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOR A VARIETY OF
                                                   .) (POTENTIAL).
.) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                         (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-4, IL-7
               (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                              a collaboration
MBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    150
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CYRG_CANFA
ID CYRG_C
AC P40321
AC P40321
DT 01-FEB
DT 01-FEB
DT 15-JUL
DE CYCOK1
DE (Inter
GN ILIRG
OS Enkary
OC Mammal
ON NCBIT
RN [1]
RN [1]
RN FEDUEN
RA Hentho
RA Fellbu
RT "IL-ZR
RT Genomi
Genomi
Genomi
CC -!-FU
CC -!-FU
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 severe combined immunodeficiency is a homologue disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P40321;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Cytokine receptor common gamma chain precursor (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL-2R gamma chain)
                                                                                                                                                                                                                                      ++
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                           EMBL; U04361; AAC48403.1; HSSP; P31785; 1ILN.
                                                                                                                                                                                                                                                                                                         Genomics 23:69-74(1994)
                                                                                                                                                                                                                                                                                                                                                    Felsburg P.J.;
                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Spleen
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYRG_CANFA
                   InterPro; IPR003531; Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1
                                                                                                                                                                                                                                                                                                                                                            Henthorn P.S., Somberg
                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95130114; PubMed-7829104;
                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9615
           PROSITE;
                                                     InterPro; IPR002996; InterPro; IPR003961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 PDLVCYTDYLQTVICILEMWNL----HPSTLTLTWQDQYEELKDEATSCSLHRSAHNATH
                                                                                                                                                                                                 INTERLEUKINS.
SUBURIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AN SUBURIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AN PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: DEFECTS IN IL2RG ARE THE CAUSE OF A CANINE X-LINKED SYSTEM COMBINED IMMUNODEFICIENCY.
SINILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                              FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LYTERVRSRYNPLCGSAOH--WSDWSYPIHWGSNTSKENIENPENP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G---CWFGKKEIRLYETFVVQLQDPREHRKQPKQMLKLQDLVIPWAPENLTLRNLSEFQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DSSYELQVRAGPMPGSSYQGTWSEWSDPVIF - - QTQSEELKEGWNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NISWRSDYEDPAFYMLKGKLOYELQYR-NRGDPWAVSPRKLISVDSR-SVSLLPLEFRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PKVQCFVFNVEYMNC---TWNSSSEPQPNNLTLHYGYRNFNGDDKLQECGHYLFSEGITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSWSNRYLDHC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQY--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
            PS01355;
Transmembrane; Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                             COMMON SUBUNIT FOR THE RECEPTORS FOR A VARIETY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
           HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                               Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%;
                                            Hematopo_receptor_S_F1.
                                                                                                                                                                                                                                                                                                                                                             R.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LEHLVQYRSDRDRSWTEQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40;
                                                                                                                                                                                                                                                                                                                                                            Fimiani V.M., Puck J.M., Patterson D.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 127.5; DB
Pred. No. 0.0004
                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Ve
; Fissipedia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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ia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
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ogue of the
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                                                                                                                                                                                                                                                                                                                                        canine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         217
                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  268
                                                                                                                                                                                                                                                                                                                              human
                                                                                                                                                                                                                                                                                                                                        X-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (P64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
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망
                                                                                                                                                                                                                                                                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL2B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DISULFID
DISULFID
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSMEM
DOMAIN
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                   Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
Fleming K., French L., Garner A.A., Gilbert
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                           217
                                                                                                                                                                                                                                                                                                                                                                                                                               173
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                                                                                                                                                                                                                                                                                                                                                                                                          KFYTFRVRSRYNPLCGSAQR--WSEWSHPI
                                                                                                                                                                                                                                                                                                                                                                                                                              KDSSYELQVRAGPMPGSSYQGTWSEWSDPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51;
                                                                                                                                    244:551-556(1989).
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23
262
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284
151
102
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102
159
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42516
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24
71
75
84
159
164
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POTENTIAL.
N-LINKED (
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N-LINKED
N-LINKED
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ILZB_HUMAN STANDARD,
P14784;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Interleukin-2 receptor beta chain precursor (
reffinity IL-2 receptor beta subunit) (C
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-89242117; PubMed-2785715;
Hatakeyama M., Tsudo M., Minamoto S., Kono T., Doi T.
Miyasaka M., Taniguchi T.;
"Interleukin-2 receptor beta chain gene: generation (
"Interleukin-2 receptor beta chain cDNA's.";
              MEDLINE-2005/165; PubMed-10591208;

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Dunham I., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,

Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.,

Bagguley C., Bailey J., Barlow K., Bates K.N., Beasley O., Bi

Blakey S., Bridgeman A.M., Buck D., Burgess J., Burrill W.D.,

Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.

Cobley V., Cole C.G., Collier R.E., Connor R.E., Conroy D., C.

Coville G.J., Cox A.V., Davis J., Dawson E., Dhami P.D., Dock

Dodsworth S.J., Durbin R.M., Ellington A., Fey J.

Dodsworth S.J., Durbin R.M., Ellington A., Fey J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDLVCYTDYLQTVICILEMWNL----HPSTLTL-TWQDQYEELKDEATSCSLHRSAHNAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -LEHVVQYRSDWDRSWTEQ-----
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Pred. No. 0.00043;
5; Mismatches 92;
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CYTOKINE RECEPTOR COMMON GAMMA CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor (IL-2 subunit) (CD122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptor) (P70-75) antigen).
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(POTENTIAL).
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) (POTENTIAL).
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                                                                                                                                                          O., Bird
                                                                                                                                                                                                                                                                                                                                                                    three receptor
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Dockree
ey J.M.,
ard M.E.,
                                                                                                                                                                                                       D.M.,
                                                                                                       S.M.
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RA Ramsey Y. Rogers L. Ross M.T. Scott C.E. Sebra H.K. Skuce C.D.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A.,
RA Smalley S., Smith M.L., Williams L., Williams S., Williams G., Williams S., Williams G., Williams S., Williams M., Walliams S., Williams M., Williams S., Williams S., Kawasaki K., Sasaki T.,
RA Miteley M.N., Willey D., Williams L., Williams S., Kawasaki K., Sasaki T.,
RA Beck S., Rogers J., Shinizu N., Minoshima S., Kawasaki K., Sasaki T.,
RA Asakawa S., Kudoh J., Shinizu N., Minoshima S., Kawasaki K., Sasaki T.,
RA Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N.,
RA Asakawa S., Kudoh J., Shang F., Fu Y., Hu P., Hua A., Kenton S.,
RA Da H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E.,
RA Da H., Lao H.I., Lewis J., Lewis S., Jin S.-P., Loh P., Malaj E.,
RA Lai H., Lao H.I., Lewis J., Lewis S., Win S.-P., Loh P., Malaj E.,
RA Nelson D., Song L., Wang Y., Wang Y., Wang Z., White J., Willingham D.,
Willingham D., Wang Y., Wang Z., White J., Willingham D.,
Willingham D., Scheet P., Wang Y., Wang Z., White J., Willingham D.,
Willingham D., Steward M., Seela D., Graves T.,
RA Rohlfing T., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K.,
RA Rohlfing T., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K.,
RA Rohlfing T., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K.,
RA Rohlfing T., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K.,
RA Rohlfing T., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K.,
RA Rohlfing T., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K.,
RA Rohlfing T., Scheet P., Walker C., Wansley A., Wohldmann P., Pepin K.,
RA Rohlfing T., Scheet P., W
                                             InterPro; IPR002996; C
InterPro; IPR003961; E
InterPro; IPR003531; E
SMART; SM00060; FN3; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pearson D., Phillimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J., Phillips S.H., Plumb R.W., Ramsay Ramsey Y., Rogers L., Scott C.E., Sehra H.K., Skuce Smallov S. Cmith M. Cosaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3D-STRUCTURE MODELLING OF 31-230.
MEDLINE-95111955; PubMed-7529123;
Bamborough P., Hedgecock C.J., Richards W.G.;
"The interleukin-2 and interleukin-4 receptors studied by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Khan A.S., Lane L., Tilahun Y., Wright H.; "The DNA sequence of human chromosome 22."; Nature 402:489-495(1999).
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                                                                                                                                                                                                                                                                                                                              entities requires a license agreement or send an email to license@isb-sib.cl
                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modelling.";
Structure 2:839-851(1994)
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                                                                                                                                                                                                   PIR; A30342; A30342.
PDB; 11LM; 26-JAN-95.
                                                                                                                                                                                                                                                   EMBL; M26062; AAA59143.1; -. EMBL; AL022314; CAA18444.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lloyd C., Lloyd D.M., Martyn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kimberley
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                                                                                                                                                   MIM; 146710;
                                                                                                                                                                              PDB; 1ILN; 26-JAN-95.
Receptor; Transmembrane; Glycoprotein; Signal;
                          PROSITE; PS01355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WITH A GAMMA CHAIN.
SUBCELULIAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
DATABASE: NAME-PROW; NOTE-CD guide CD122 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd122.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: RECEPTOR FOR INTERLEUKIN-2. THIS BETA SUBUNIT IS
INVOLVED IN RECEPTOR MEDIATED ENDOCYTOSIS AND TRANSDUCES THE
MITOGENIC SIGNALS OF IL-2.
SUBUNIT: NON COVALENT DIMER OF AN ALPHA AND A BETA CHAINS. IL-2R
EXIST IN 3 DIFFERENT FORMS: A HIGH AFFINITY DIMER, AN INTERMEDIATE
AFFINITY MONOMER (BETA CHAIN), AND A LOW AFFINITY MONOMER (ALPHA
CHAIN). THE HIGH AND INTERMEDIATE AFFINITY FORMS ALSO ASSOCIATE
                                                                                                                                                                                                                                                                                                                                 an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.W., Ho
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                                                                                                                                                                                                                                                         CAA18444.1; -.
                        HEMATOPO_REC_S_F1; 1.
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                                                                        Hematopo_receptor_S_F1
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                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                 Usage
  3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 collaboration -
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C.D.,
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В
RESULT 15
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Best Local S
Matches 51
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DISULFID
CARBOHYD
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CARBOHYD
SEQUENCE
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P16871;
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CHAIN
DOMAIN
                                                                                    -:- FUNCTION: RECEPTOR FOR INTERLEUKIN-7.
-:- SUBGUNT: HETERODIMER OF AN ALPHA CHAIN AND A COMMON GAMMA CHAIN.
-:- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN AND ALSO SECRETED.
-:- ALTERNATIVE PRODUCTS: 3 ISOFORMS; H20 (SHOWN HERE), H1 AND
-:- H6/SECRETED; ARE PRODUCED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-:- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-:- SIMILARITY: ONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-:- DATABASE: NAME-PROW; NOTE-CD guide CD127 entry;
WWW-"http://www.ncbi.nlm.nih.gov/prow/dd/cd127.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-AUG-1990 (Rel. 15, C
01-AUG-1990 (Rel. 15, I
16-OCT-2001 (Rel. 40, I
Interleukin-7 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                               This
                                                                                                                                                                                                                                                                                                                                                    Goodwin R.G., Friend D., Ziegler S.F., Jerzy R., Falk B.A., Gimpel S., Cosman D., Dower S.K., March C.J., Namen A.E., Park "Cloning of the human and murine interleukin-7 receptors: demonstration of a soluble form and homology to a new receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=B-cell;
MEDLINE=90199875;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                           superfamily."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     213 LQGEF--TTWSPWSQPLAFRTKPAALGKDTIPWLGH 246
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                      SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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Pred. No. 0.00087;
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EXTRACELLULAR
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Best Local Similarity
Matches 42; Conserv
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PIR; A34791; A34791.
PIR; B34791; B34791.
PIR; C34791; C34791.
MIM; 146661; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
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204 KVRS--IPDHYFKGFWSEWSPSYYFRT 228
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                                                                                                                                                                                                                                                                                                            SHLQKKYVKV---LMHDVAYRQEKDENKWT-----HVNLSSTKLTLLQRKLQPAAMYEI 203
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PHOSPHORYLATION (BY PKC) (POTENTIAL).
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PPPFSLQSGILTLNPYAGGGPLITSLGSNQEEAYVTMSSFY
QNQ -> VSVFGA (IN ISOFORM H1).
OFDE4C84481B6B38 CRC64;
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; Sequence 115, Application US/09522217
; Patent No. 6307024
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CURRENT FILING DATE: 2000-03-09
EARLIER APPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-09
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: No. 6307024ak, Julia E
APPLICANT: Presnell, Scott R.
APPLICANT: Sprecher, Cindy A.
APPLICANT: Foster, Donald C.
APPLICANT: Holly, Richard D.
APPLICANT: Gross, Jane A.
APPLICANT: Johnston, Janet V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 115
LENGTH: 538
TYPE: PRT
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Sequence 97, Applica Patent No. 6307024 GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL CYTOKINE ZALPHA11 LIGAND
FILE REFERENCE: 99-16
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                                                                                                                                                                                                                                                                                                                                                                              Local Similarity es 218; Conserv
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                                                                                                                     VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH
                                                                                                                                                                                  SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                       Application US/09522217
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EARLIER PILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEO ID NOS: 115
SOFTWARE: FASTSEQ for Windows Version 3.0
SEO ID NO 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: No. 6307024ak, Julia E APPLICANT: Presnell, Scott R. APPLICANT: Sprecher, Cindy A. APPLICANT: Foster, Donald C. APPLICANT: Holly, Richard D. APPLICANT: Gross, Jane A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 218; Conserv
                                                                                                                                                                                                                                                                                                                sequence 2, Application US/08599455B
Patent No. 5972621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Nelson, Andrew J.
APPLICANT: Dillon, Stacey R.
APPLICANT: Hammond, Angela K.
MITLE OF INVENTION: NOVEL CYTOKINE ZALPHAIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gross, Jane A. APPLICANT: Johnston, Janet V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLING FILING DATE: 1999-03-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/522,217
                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT \
ORGANISM: Arti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                           APPLICANT: Tartaglia, Louis A.
APPLICANT: Tepper, Robert I.
APPLICANT: Tepper, Janice A.
APPLICANT: Culpepper, Janice A.
TITLE OF INVENTION: METHODS OF IDENTIFYING COMPOUNDS TITLE OF INVENTION: MODULATE BODY WEIGHT USING THE OB
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
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ZIP: 02110-2804
                                                                                             STATE:
                                                                                                                             STREET:
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100.0%; Pred. No. 8.5e-123;
type 0; Mismatches 0;
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Copyright (c) 1993 - 2000 Comp
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US-09-522-217-2
US-09-522-217-85
US-09-522-217-89
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US-09-522-217-72
US-08-522-217-72
US-08-33-305-3
US-08-726-817-3
US-08-726-817-3
US-08-726-913-3
US-08-794-524-3
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Best Local Similarity
Matches 162; Conserv
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Database

Result

TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162

TCPSCDSYEKKPPKEFLERFKSLLQKMIHQHLSSRTHGSEDS 162

LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120

100.0%; (ilarity 100.0%;) (Conservative 0;

Score 850; DB 4; Pred. No. 4.8e-87; Mismatches 0;

Length 162; Indels

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Gaps

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LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120

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ALIGNMENTS	PCT-US94-03793-5 PCT-US96-0423-2 US-08-031-399-3 US-08-726-017-6 US-08-725-969-6 US-08-725-969-6 US-08-725-969-6 US-08-725-969-6 US-08-725-969-3 US-08-725-969-5 US-08-725-969-5 US-08-725-917-5 US-08-725-917-5 US-08-726-917-5 US-08-726-917-5 US-08-726-917-5 US-08-726-917-5 US-08-726-95-5 US-08-726-95-5 US-08-726-95-5	
	Sequence 5, Appli Sequence 2, Appli Sequence 3, Appli Sequence 6, Appli Sequence 3, Appli Sequence 3, Appli Sequence 5, Appli	

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GENERAL INFORMATION:
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: No. 6307024ak, Julia E.
APPLICANT: Presnell, Scott R.
APPLICANT: Sprechez, Cindy A.
APPLICANT: Sprechez, Cindy A.
APPLICANT: Foster, Donald C. *
APPLICANT: Holly, Richard D.
APPLICANT: Holly, Richard D.
APPLICANT: Hammond, Angela K.
APPLICANT: NUMBER: US/09/522,217
CURRENT TALING DATE: 2000-03_09
EARLIER REPLICATION NUMBER: US 60/123,547
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/123,904
EARLIER APPLICATION NUMBER: US 60/142,013
EARLIER FILING DATE: 1999-07-01
NUMBER OF SEQ ID NOS: 115
SOSTWHARE: FRASTSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 1
US-09-522-217-2
; Sequence 2, Application US/09522217
. barent No. 6307024
; TYPE: PRT
; ORGANISM: Homo
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RESULT
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Best Local Similarity 100.0%;
Matches 218; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in particular T-lymphocyte-related disorders including atopic conditions such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic inflammatory diseases and graft verses host disease, disorders Anvolving the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney disorders including polycystic kidney disease, cystic renal dysplasia, disorders of the thymus including lymphomas, Hodgkin disease and carcinoids. The 16445 polypeptides are also useful as modulating agents in cellular processes including growth promoting activity particularly the antigen-independent proliferation of T-helper cell cyones. The encoding nucleic acid is useful as primers or hybridization probes for the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for tissue typing and in forensic biology. The present sequence represents the human IL-9/IL-2 receptor-like polypeptide (AAH16445).
                                                                                                                                                    09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                       OMYZ)
                                                                                                                                                                                                                                                   14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                           zalphall ligand; cytokine;
tumourigenesis; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB18629;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB18629
                               N-PSDB; AAA75609
                                                                                                                                                                                                                   09-MAR-2000,
                                                                                                                                                                                                                                                                                WO200053761-A2
                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of/MBP-human zalphall ligand fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                         22-JAN-2001
                                                                            Johnston JV,
                                                                                         Novak
                                                                                                                                                                                                                                                                                                                Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VRAGPMPGSSYQGTWSEWSDPVIFQTQSBELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cpdlvcytdylqtvicilemwnlhpstltltwqdqyeglkdeatscslhrsahnathaty 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vragpmpgssyggtwsewsdpvifqtgseelkegwnph 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tchmdvfhfmaddifsvnitdqsgnysqecgsfl/laesikpappfnvtvtfsgqyniswr
                                               2000-565600/52
                                                                                         JE,
                                                                                                                        / ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            538 AA;
                                                                          Presnell SR,
V, Nelson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entr/
                                                                                                                                                                                                                   2000WO-US06067
                                                                                                                                                    99US-0264908.
99US-0265992.
99US-0142013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein;
designated zalphall ligand, useful for stimulating
                                                                          Sprecher CA,
Dillon SR,
                                                                                                                                                                                                                                                                                                                                                           haematopoietic cell proliferation; hematopoiesis; B cell tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /606 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1195; DB 22/
Pred. No. 1.6e-115;
Mismatches //;
                                                                            Foster
Hammond
                                                                            AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                         Holly RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538;
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                                                                                                                                                                                                                                                                                                                                                                           lymphoma;
                                                                                          Gross JA;
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New human cytokine,

23-SEP-1999;

99WO-US22149

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RESULT 10
AAY79316
ID AAY7933
XX AC AAY793
AC AAY793
XX IN-
DE MAltos
XX Cytoki
KW Cytoki
KW apopto
KW infect
XX Infect
XX Protei
FT Protei
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a MBP-human zalphall ligand fusion. CC Zalphall ligand is a cytokine. The zalphall ligand is yeeful for CC Stimulating the proliferation and development of haematopoietic cells in vitro and in vivo. Zalphall ligand polynucleotides can be used as CC primers or probes for cloning the zalphall gene. The zalphall ligand color is useful for treating tumourigenesis. A zalphall ligand-saporin fusion CC toxin may be used for treating leukaemias and Ymmphomas. Antagonists CC against zalphall ligand are useful as research reagents for CC characterizing ligand-receptor interaction, Antagonists are also useful CC characterizing leyand-receptor interaction, Antagonists are also useful CC characterizing leyand-receptor interaction, Antagonists are also useful CC characterizing expansion, proliferation, Activation and differentiation CC colls involved in regulating hematopolesis. The zalphall ligand may CC virus, a parasite or a bacterium. The zalphall polypeptides, CC polynucleotides, antagonists, agonists and antibodies are also useful CC for the detection, diagnosis, prevention, and treatment of diseases CC associated with a zalphall ligand genetic defect.
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and
                                                                                                                                                                                                                                     Cytokine receptor; zalphall; maltose binding protein; human; apoptosis; signal transduction; growth factor; cancer; tumou infection; gene therapy; diagnosis; huzalphall/MBP-6H.
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                                                                                                                                                                                                                                                                                                                                                                                AAY79316;
                                                                                                                                                                                                                                                                                                                                                                                                                 AAY79316 standard;
                                                                                                                    Protein
                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                             Maltose binding protein-zalphall fusion
                                                                                                                                                                                                                                                                                                                                               18-JUL-2000
                                    30-MAR-2000.
                                                                   WO200017235-A2
                                                                                                                                                       Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proliferation and/or development of haematopoietic cells in in vivo, and for treating tumourigenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vragpmpgssyqgtwsewsdpvifqtqseelkegwnph 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218;
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                  /note= "maltose binding protein\"
389..606
                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   Protein; 606
                                                                                                      "zalphall cytokine binding
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Pred. No. 1.9e-115;
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                                                                                                        domain"
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09-MAR-1999;
06-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression plasmid containing huzalphall/MBP-6H DNA (see AAZ9454) was constructed via homologous recombination and the fusion protein was expressed in Escherichia coll BL21 using vector plasmid prapels. Zalphall may be involved in an apoptotic cellular pathway, or is a cell-cell signalling molecule, growth factor receptor, or extracellular matrix associated protein with growth factor hormone activity. The invention provides zalphall polypeptides (including fusion proteins), polynuclectides and antibodies, and methods for their use in the treatment and diagnosis of conditions associated with altered zalphall expression or activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel nucleic acid encoding zalphall e.g. viral infection or tumors, and stimulate cell proliferation -
         Human; anticancer; anti-inflammatory; immunosuppressive; antiallergi antiasthmatic; antirheumatic, antiarthritic; nootropic; vasotropic; neuroprotective; antibacterial; cerebroprotective; osteopathic; nephrotropic; hypotensive; hypertensive; antifungal; anti-HIV; antiprotozol; antiviral; antianemic; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is that of a fusion protein, designat huzalphall/MBP-6H, comprising a maltose binding protein (w fused to the cytokine binding domain (amino acids 20-237) human class I cytokine receptor zalphall (see AAY79312).
                                                                                                     Human HNOVYLR
                                                                                                                                  08-AUG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                                             AAY94304 standard; Protein; 538
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                                                                                                                                                                                                                                                                                    VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                           SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                     218;
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                                                                                                                                                                                                                                                                                                                           {\tt sdyedpafymlkgklqyelqyrnrgdpwavsprrklisvdsrsvsllplefrkdssyelq}
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   disease; Alzhe
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                                                                                                                                  (first entry)
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99US-0265117.
99US-0347930.
                                                                                                     polypeptide 1.
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   disease;
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Pred. No. 1.9e-115;
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7) of
                                                                        antiallergic;
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC be a member of the Nytokine receptor family of polypeptides. It shows to have similar biological functions/properties. The polynucleotide may be obtained from a cDNA library derived from mRNA in cells of human been compared to the synthesised using compercially available techniques. The growth, cen be synthesised using compercially available techniques. The growth, ce interaction of cytokines and their cognate receptors. Thus the continue and its product are useful for diagnosing or treating a wide range of disease, saltery astimation, autoimmune continues, crohn's disease, altery astimation, autoimmune continues, crohn's disease, altery astimation, autoimmune continues, crohn's disease, saltery astima, rheumatoid arthritis, cardiovascular disease, kidney disease, multiple sclerosis, osteoarthritis, compocardial infarction, hypotension, hypotresion, acquired immune deficiency syndrome (AIDS), male pattern baldness, and bacterial, con formula infarction, so treating and continues and continues of continues and continues of continues and continues of cardiovascular disease, kidney disease, instriple sclerosis, osteoarthritis, convocardial infarction, hypotrension, hypotrension, acquired immune convocation, protozoan and viral infactions.
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      multiple sclerosis; cancer; infection; cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a HNOVILR polypeptide which is be a member of the Wtokine receptor family of polypept homology with human interleukin receptor 2 and is there
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 30\31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lated polypeptide of HNOVILR type used for diagnosing or treating example cancer, inflammation, autoimmune disease.
                                                                                                                                                                                                                                                                                                            CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSSSLHRSAHNATHATY
                                                                                                                                                                                                                                         TCHMDVFHFMADDIFSVNITDOSGNYSQECGSFLLAESIKPAPPFNVTVÅRSGQYNISWR 120
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                                                                                   vragpmpgssyggtwsewsdpvifqtqseelkegwnph
                                                                                                                      VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
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ALIGNMENTS

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DR EMBL; AF254067; AAG29346.1; -.
DR EMBL; BC004348; AAH04348.1; -.
DR InterPro; IPR003961; FN_IIII.

7R SMART; SM00060; FN3; 1.

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01-MAR-2001
01-JUN-2001
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"Interleukin 21 and its receptor are involved in NK cell expansion and regulation of lymphocyte function.";
Nature 408:57-63(2000).
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Horia; Chordata; (
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OZAKİ K., KİKİY K., MİChAlovich D., Young
"Cloning of a type I cytokine receptor mo
receptor beta chain.";
Proc. Natl. Acad. Sci. U.S.A. 97:11439-11
EMBL; AF269133; AAC23419.1; -.
InterPro; IPR003961; FN_III.
SMART; SM00060; FN3; 1.
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Q9ESM1;
Q9ESM1;
01-MAR-2001
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Parrish Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,
Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,
Burkhead S., Heipel M., Brandt C., Kuijper J.L., Kramer J.,
Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hambly K.
Mudri S., Clegg C., Moore M., Grant F. J., Lofton-Day C., Gilbert T
Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,
Maurer M., Kaushansky K., Holly R.D., Foster D.;
"Interleukin 21 and its receptor are involved in NK cell expansion
regulation of lymphocyte function.";
Nature 408:57-63(2000).
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Donaldson D.D., Whitters M.J., Fitz L., Unger M., Finner
Donaldson D.C., Lowe L., Wood C.R., Young D.A., Collins M.
Dagdigian C., Lowe L., Wood C.R., Young D.A., Collins M.
"Chromosome 16p12 Encodes a Biologically Active IL-2Rb F
Receptor with Lymphoid Restricted Expression.";
Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF269134; AMGD; MGI:1890475;
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OZAKI K., Kikly K., Michalovich D., Young P.R., Leonard W.J.
"Cloning of a type I cytokine receptor most related to the I receptor beta chain.";
Proc. Natl. Acad. Sci. U.S.A. 97:11439-11444(2000).
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Mammalia; Eutheria;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
LYMPHOCYTE RECEPTOR BETA (INTERLEUKIN 21 RECEPTOR)
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                                                                                                                                                VRAAPQPGTSFRGTWSEWSDPVIFQTQAGEPEAGWDPH
                                                                                                                                                                                        VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                   SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEERKDSSYELQ
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                                                                                                                                                                                                                                    SAYDEPSNYVLRGKLQYELQYRNLRDPYAVRPVTKLISVDSRNVSLLPEEFHKDSSYQLQ
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Metazoa; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chordata; Chord
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31; Mismatches
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Sciurognathi; Muridae;
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Matches 149
           Gebicke-Haerter P.J.; to the Submitted (JTL-1997) to the EMBL; S79263; AAB35068.1; ~. EMBL; AJ000555; CAA04186.1; InterPro; IPR002996; CRIA.
                                                                                                                  SEQUENCE FROM N.A.

MEDLINE=95370942; PubMed=7643220;

Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;

"Cloning of rat interleukin-3 receptor beta-subunit from microglia and its mRNA expression in vivo.";

J. Neurosci. 15:5800-5809(1995).
                                                                                                                                                                                                                                                                         064146;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT)
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Mammalia; Eutheria;
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"A novel cytokine receptor NR8 is
Polymorphism in Balb/c mouse.";
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Mammalia; Eutheria;
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Best Local
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Best Local
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Q9Z1A0;
Q1-MAY-1999
Q1-MAY-1999
Q1-DEC-2001
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NON_TER
NON_TER
                                                                                                                                                                                                                                                                                 Receptor. SEQUENCE
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"Guinea pig ILS receptor bet

Submitted (MAR-1997) to the

EMBL; U94688; AAC77520.1; -.

HSSP; P40189; 1BQU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
Logsdon N.J., Graham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00041; fn3; SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1999 (TrEMBLrel. 10, 01-MAY-1999 (TrEMBLrel. 10, 01-DEC-2001 (TrEMBLrel. 19, INTERLEUKIN-5 RECEPTOR BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR003961; FN_III
InterPro; IPR003531; Hemato
                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00041; fn3; SMART; SM00060; FN3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10141;
[1]
                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
310
                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
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                                                                                    250
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                                                                                                                           3 DLVCYTDYLOTVICILEMWNLHPSTLTLTW-----
QI-RVSNPRPHSQYT-
                                       SLHRSAHNATHATYTCHMDVFHFMADDIFSVNITDQSG-NYSQECGSFLLAESIKPAPPF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLHTCNLWVTLEPKLFLPNSIYVARVRAQLAPGSSLSGRPSGWSPEVHWDSPTED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HRCVPRRCVLPYTQFSVSKEDYYSLQPDRDLSIHLV-------VPLAQHVQPPPP
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                                                                                                                                                                        Similarity 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                             PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                          IPR002996; CR1A.
IPR003961; FN_III.
IPR003531; Hematop
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ω.
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26.5%;
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Last annotation updat
CHAIN.
                                                                                                                                                                     Score 155.5; !
Pred. No. 8.6e
33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
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Pred. No. 1.7e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hystricognathi;
                                                                                                                                                                                                                                                                                   D43FB1CA88525536 CRC64;
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                                                                                                                                                                                               155.5;
No. 8.
-VTVRPRNGEKFIRSANHIQMA---
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                                                                                                                                                                                                                  DB 11;
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                                                                                                                -QDQYEELKDEAT--SC
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RESULT
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AC Q6
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Best Local
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Q9QWG3;
Q1-MAY-2000 (TrEMBLrel. 1
Q1-MAY-2000 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
Q1-DEC-7001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                   atches
                                                                                                                                                                                                                                                                                                                                                                                                                                     Joost H.G.;

"Hyperleptinemia and leptin receptor variant Asp600Asn in the obese, "Hyperleptinemic KK mouse strain.";

J. Endocrinol. 21:337-345(1998).

EMBL; V10296; CAA71342.1; -.

HSSP; P16471; 1BP3.

MGD; MGI:104993; Lepr.
InterPro; IPR003961; CRIA.
InterPro; IPR003961; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.

InterPro; IPR003531; Hematopo_receptor_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
STRAIN-KK OBESE: TISSUE-BRAIN, HYPOTHALAMUS;
Igel M., Taylor B.A., Phillips S.J., Becker
Q62960 PRELIMINARY;
Q62960;
Q1-NQV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                     prosite; ps01353; hematopo_rec_l_r2; unknown_1.
prosite; ps01355; hematopo_rec_s_r1; unknown_1.
                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00041; fn3; 3.
SMART; SM00060; FN3; 3
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                                                                                               327
                                                                                                                      205
                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                                          39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYS 87
                                                       æ
                                                                                                                    QTQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPPLE -- PATTYLARVRVKPSPGGAYNGIWSEWSE 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVS 165
                                                                                             TTO
                                                                                                                                              T--IVREAAEIVSATSLLVDSVLP----GSSYEVQVRSKRLDGS
                                                                                                                                                                                                                         QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG
                                                                                                                                                                                                                                                   LKDSFQTVQCNCSLRGC-----ECHVPVPRAKLNYALLMYLEITSAGVSFQSPLMS
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                                                                                                                                                                        DPWAVSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF 204
                                                                                                                                                                                                 LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYLENS
                                                                                                                                                                                                                                                                                                   l Similarity
57; Conserv
                                                                                                                      207
                                                                                             329
                                                                                                                                                                                                                                                                                                                                                                 1162 AA;
                                                                                                                                                                                                                                                                                                    Conservative
                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                 600 N -> D.
; 130787 MW; 541E77CBB46EC00D CRC64;
                                                                                                                                                                                                                                                                                                 12.1%; Score 144; Di
31.1%; Pred. No. 1.76
tive 22; Mismatches
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19,
      01,
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      Created)
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                                PRT;
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                                895
                                                                                                                                                                                                                                                                                                                DB 11;
1.7e-05;
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                                                                                                                                                 -GVWSDWSSPQVF
                                                                                                                                                                                                                                                                                                   44;
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TEPTIN RECEPTOR.
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Best Local Similarity
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InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
pfam; pf00041; fn3; 2.
smarr; sm00060; FN3; 1.
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Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel.
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LEPTIN RECEPTOR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
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fatty rats."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10116;
SEQUENCE FROM N.A.

MEDLINE-97215244; PubMed-9061609;

Luoh S.M., Di Marco F., Levin N., Armanini M., Xie M.H., Nelsor

Luoh S.M., Di Marco F., Levin N., Gurney A., de Sauvage

Bennett G.L., Williams M., Spencer S.A., Gurney A., de Sauvage
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
Eukaryota; Metazoa; (
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Pred. No. 4.8e-05;
3; Mismatches 62;
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Sciurognathi; Muridae;
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Catarrhini;
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
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                                             Nelson
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              F.J.;
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EMBL; U66495; AAB07495.1; ...

EMBL; U50748; AAC23650.1; -..

HSSP; P16471; 1BP3
InterPro; IPR00296; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.

Pfam; PF00041; fin; 2.

SMART; SM00060; FN3; 1.
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"A role for leptin and its cognate receptor Curr. Biol. 6:1170-1180(1996).
EMBL; U66496; AABD7496.1; -.
HSSP; P16471; 1BP3.
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01-FEB-1997
01-FEB-1997
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SEQUENCE FROM N.A.
MEDLINE=96398968; PubMed=8805376;
Le B. Solar G.P., Yuan J.Q.,
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LEPTIN RECEPTOR.
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InterPro;
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J. Wol. Endocrinol. 18:77-85(1997).
                                                                                                                                                                                                                                            Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
SEQUENCE 896 AA; 102489 MW; D371C7A4186DEEF3 CRC64;
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IPR003961; FN_III.
IPR003529; Hematopo_receptor_L_F2.
IPR003531; Hematopo_receptor_S_F1.
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                                                                         Conservative
                                                                                                                                                                                                    109392 MW;
                                                                                              11.5%; Score 137; DB 4; 28.0%; Pred. No. 6.6e-05;
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28.0%; Pred. No. 6e-05;
Live 25; Mismatches
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Last sequence update)
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Q92921;
01-FEB-1997 (TrEMBLrel. C
01-FEB-1997 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. 1
                                                                   013594 PRELIMINARY; PRT; 896 AA. 013594; O1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat B219/OB RECEPTOR ISOFORM HUB219.3 PRECURSOR. Homo sapiens (Human)
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SEQUENCE
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InterPro; IPR003961; FN_III.
InterPro; IPR003961; FN_III.
InterPro; IPR003531; Hematopo_receptor_S_F1.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN_1.
PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
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EMBL; U66497; AAB07497.1; -.
HSSP; P16471; 1BP3
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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47; Conserv
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                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
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RESULT Q13593 Q13593 Q1 AC Q1 DT Q1 DT Q1 DT Q1 DT Q1 DT Q1 DT Q1 DT Q5 HC QC Et QC K
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Best Local Similarity
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
B219/OB RECEPTOR ISOFORM HUB219.2 PRECURSOR.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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SMART; SM00060; FN3; 1.
PROSITE; PS01355; HEMATOPO_REC_L_F2;
PROSITE; PS01355; HEMATOPO_REC_S_F1;
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Nat. Med. 2:585-589(1996).
EMBL; U52914; AAC50511.1; -.
HSSP; P16471; 1883.
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SEQUENCE FROM
SEQUENCE
                                                         Signal; Receptor.
                                                                                                     Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2;
PROSITE; PS01355; HEMATOPO_REC_S_F1;
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Nat. Med. 2:585-589(1996).
EMBL; U52913: AAC50510.1; -.
HSSP; P16471; 18P3.
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InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2
InterPro; IPR003531; Hematopo_receptor_S_F1
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                                 CHAIN
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IPR003961; FN_III.
IPR003529; Hematopo_receptor_L_F2.
IPR003531; Hematopo_receptor_S_F1.
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896 AA;
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102516 MW;
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Pred. No. 7
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          POTENTIAL.
B219/OB RECEPTOR ISOFORM HUB219.2.
4; 6D51126F33076626 CRC64;
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Best Local S
Matches 38
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Best Local 9
                 Q96P01;
Q96P01;
01-DEC-2001
01-DEC-2001
01-DEC-2001
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Platika D., Snodgrass                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q13592 PRELIMINARY; PRT; 958 AA. Q13592; Q1-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation update) B219/OB RECEPTOR ISOFORM HUB219.1 PRECURSOR.
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SEQUENCE
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InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; In3; 2.
SMART; SM00060; FN3; 1.
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Mammalia; Eutheria;
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PROSITE; PS01355; HEMATOPO_REC_S_F1; UNKNOWN_1.
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INTERLEUKIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity 33.9
38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22
958 AA;
                 (TrEMBLrel. 19, (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                        PRELIMINARY;
  RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 POTENTIAL.
958 B219/OB RECEPTOR ISOFORM HUB219.1.
109419 MW; C7E0E8D18428677B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             11.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.4%; 33.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           18;
                       Last sequence update)
Last annotation update)
                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 136; DB 4;
Pred. No. 8.3e-05;
8; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 136; DB 4;
Pred. No. 7.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vo
Catarrhini;
                                                                                                                        PRT;
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                                                                                                                        825
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i; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 958
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A.;

Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AF421855; AAL12163.1; -.

Receptor.

Receptor.

825 AA; 89644 MW; 9ADF725A38F9FB5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IL4R.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9806;
[1]
                                                               181 EPSLRIAASTLKSGISYRARVRAW---AQCYNTTWSEWS 216
                                 170 E-----FRKDSSYELQVRAGPMPGSSYQGTWSEWS 199
                                                                                                                                 61 TCHMDVFHFMADDIFSVNITDQSGNYSQEC------GSFLLAESIKPAPPFNVTV-- 109
                                                                                                                                                                                                  34 CVSDYMSISTC---EWKMNGPTNCSTELRLLYQLVF--LLSEAHTC----VPENNGGAGC 84
                                                                                                                                                                                                                       6 CYTDYLQTVICILEMWNLHPST-----LTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
                                                                                                                                                                                                                                                                   12;
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Search completed: June 28, 2002, 07:44:32 Job time: 227 sec

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Title:
Perfect score:
Sequence:
                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
Database
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein search, using sw model
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PIR_71:*
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1195
1 CPDLVCYTDYLQTV:
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                      283138 seqs, 96089334 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                     CPDLVCYTDYLQTVICILEM.....SDPVIFQTQSEELKEGWNPH 218
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

pir1:*
pir2:*
pir3:*
pir4:*

SUMMARIES

44	42 43	40 41	39	38	37	36	35 5	34	<u>ω</u>	32	3	30
100.5 99.5	103 102	105 104	105.5	105.5	105.5	105.5	106	108.5	110.5	112.5	113.5	113.5
8.4	& & 5 6	8.8 8.7	8.8	8.8	8.8	8.8	8.9	9.1	9.2	9.4	9.5	9.5
265 507	508 468	522 638	638	460	440	279	638	468	918	917	800	284
H 2	2 1	20	2	2	N	N	N	ш	N	N	Н	Ν
S14081 A32385	ZUHUR A45268	B45268 B28176	A33505	JL0145	JL0144	в32985	S12136	A41242	A36337	149699	S31575	S27931
erythropoietin rec erythropoietin rec	erythropoietin rec interleukin-9 rece	interleukin-9 rece somatotropin recep	somatotropin recep	interleukin-6 rece	interleukin-6 rece	somatotropin-bindi	somatotropin recep	interleukin-6 rece	membrane glycoprot	glycoprotein 130 -	interleukin-4 rece	Env/v-mpl fusion p

ALIGNMENTS

RESULT I56563

Interleukin-3 receptor beta-subunit - rat
C;Species: Rattus sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C;Accession: 15653
R;Appel, K; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J.
J. Neurosci. 15, 5800-5809, 1995
A;Ritle: Cloning of rat interleukin-3 receptor beta-subunit from cultured mi
A;Reference number: 156563; MUID:95370942
A;Accession: 156563

cultured microglia

A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-896 <RES>

RESULT 2 A40091 A40091 A40091 C;Speciles: Mus musculus (house mouse) C;Speciles: Mus musculus (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 C;Accession: A40091; A43022 R;Itoh, N; Yonehara, S.; Schreurs, J.; Gorman, D.M.; Maruyama, K.; Ishii, A.; Yahara Science 247, 324-327, 1990	OY 105 ENVTVTESG-QYNISWRSDYEDPAFYMLKGK-LQYELQYRNRGDPWAVSPRRKLISVDSR 162	Query Match 13.6%; Score 162.5; DB 2; Length 896; Best Local Similarity 25.1%; Pred. No. 2.3e-06; Matches 59; Conservative 32; Mismatches 89; Indels 55; Gaps 9; Qy 4 LVCYTDYLQTVICILEMWNLHPSTLTLTWODQYEELKDEATSCSL	A;Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955 C;Genetics: A;Gene: xIL-3Rbeta A;Gene: xIL-3Rbeta C;Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology C;Keywords: cytokine receptor F;39-235/Domain: cytokine receptor homology <crs1> F;253-433/Domain: cytokine receptor homology <crs2></crs2></crs1>
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C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology C:Keywords: cytokine receptor; duplication; transmembrane protein F:1-22/Domain: signal sequence #status predicted <SIG>F:23-878/Product: interleukin-3 receptor beta chain #status predicted <MAT>F:23-840/Domain: extracellular #status predicted <EXT>F:23-440/Domain: cytokine receptor homology <CRS1>
54-433/Domain: cytokine receptor homology <CRS2>
141-62/Domain: cytokine receptor homology <CRS2>
141-62/Domain: cytokine #status predicted <TMN>
                                                                                                                                                     A:Experimental source: splice form Re; tissue hypothalamus
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, February
C:Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439,
C:Genetics:
                                                                                                                                                                                                                                                                                                                             R;Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh, Nature 379, 632-635, 1996
A;Title: Abnormal splicing of the leptin receptor in diabetic mice. A;Reference number: $68437; MUID:96231997
A;Accession: $68441
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A;Residues: 1-815,'Q',817-878 <GOR>
A;Cross-references: GB:M29855; NID:g198342; PIDN:AAA39295.1; PID:g309406
C;Comment: In mice there are two classes of high-affinity IL-3 receptors. One contains
                                                                                                              A;Gene: Ob-Re
C;Keywords: a
                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-805 < LE
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A; Residues: 1-878 < ITO>
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A;Status: nucleic acid sequence not shown
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                                                                                                                                                                                                                                          A;Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          tin receptor, splice form Ob-Re - mouse pecies: Mus musculus (house mouse)
Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
                         Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: S68441
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Best Local
      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RRKLISVDSRSVSLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQTQ 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KLMWSECPSSHRCVPRRCVIPYTRFSNGDNDYYSFQPDRDLGIQL------MVP 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------HRSAHNATHATYTCHM----DVFHFMADDIFSVNITDQSGNYSQECGSFL 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SSLHTSNFQVNLEPKLFLPNSIYAARVRTRLSAGSSLSGRPSRWSPEVHWDSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAQHVQPPPPKDIHISPSGDHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRLQDSWEDA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAESIKPAPPFNVTVTFSG-QYNISWRSDYEDPAFYMLKGK-LQYELQYRNRGDPWAVSP 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LECYNDYTNRIIC-----SWADTEDAQGLINMTLLYHQLDKIQSVSCELSE 82
                                                                                                              alternative splicing; appetite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
    57; Conserv
                                                                                                                                                                                                                                                                    1-805 <LEE>
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      Conservative
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                    12.1%; Score 144; DB 2;
31.1%; Pred. No. 9.1e-05;
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    22;
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Pred. No. 8.
    Mismatches
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.3e-05;
es 91; Indels
    60;
                                         Length 805;
    Indels
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  44;
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  Gaps
  11;
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                                                                                                                                                                                                                                                                                                                                                                                                                       J.I.;
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PIR:S68
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R;Lee, G.H.; Proenca, R.; Montez,
Nature 379, 632-635, 1996
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A; Gene: Ob-Rc
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A; Residues: 664-892 <LEE1>
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  leptin
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                                                                                                              327 TTQ
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                                                                                                                                                                                                                                                                                         228 LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF--
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receptor, splice
                                                                                                                                                                                                                                                                                                                                  88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.1%; Score 144; DB 2; 131.1%; Pred. No. 0.0001; 37: Mismatches 60;
    torm
    Ob-Ra
    mouse
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A;Molecule type: mRNA
A;Residues: 1-796, 'GMCTVLFMD' <LEEZ>
A;Residues: 1-796, 'GMCTVLFMD' <LEEZ>
A;Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A;Cross-references: EMBL:U49110; NID:g1195492; PIDN:AAC52424.1; PID:g1195493
A;Cross-reference: splice form Re; tissue hypothalamus
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
A;Note: this sequence from splice form Re is included to produce a complete sequence
C;Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           leptin receptor, splice form Ob-Rc - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:U49108; NID:g1195488; PIDN:AAC52422.1; PID:g1195489
A;Experimental source: splice form RC; tissue hypothalamus
A;Note: the nuclectide sequence was submitted to the EMBL Data Library, February
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: nucleic acid sequence not shown; translation not shown
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277 T--IVREAAEIVSATSLLVDSVLP-----GSSYEVQVRSKRLDGS---GVWSDWSSPQVF
                                                                                      146 DPWAVSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 DPWAYSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 277 T--IVREAAEIVSATSLLVDSVLP-----GSSYEVQVRSKRLDGS----GVWSDWSSPQVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   228 LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYLENS 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYS 87
                                                                                                                                                                                                                                                                                  QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG
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                                                                                                                                                                                                                                                                                                                                                                                  -----ECHVPVPRAKLNYALLMYLEITSAGVSFQSPLMS 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.M.; Carroll, K.M.; Darvishzadeh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2; Length 892;
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                                                                                                                                                                                           -PLQYQVKYLENS
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A; Molecule type: mRNA
A; Residues: 1-896 <GOR>
A; Residues: 1-896 <GOR>
A; Cross-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
C; Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3
C; Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C; Keywords: cytokine receptor; duplication; transmembrane protein
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 23-896/Product: cytokine receptor common beta chain #status predicted <MAT>
F; 23-441/Domain: extracellular #status predicted <EXT>
F; 33-441/Domain: cytokine receptor homology <CRS1>
F; 53-434/Domain: cytokine receptor homology <CRS2>
F; 53-434/Domain: cytokine receptor homology <CRS2>
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C;Date: 31-Dec-2000 #sequence_revision 31-Dec-2000 #text_change 31-De
C;Accession: S68437
R;Lee, G.H.; Proenca, R.; Montez, J.M.; Carroll, K.M.; Darvishzadeh,
Nature 379, 632-635, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytokine receptor common beta chain precursor - mouse c;Species: Mus musculus (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change Accession: A35782
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A35782
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A;Accession: S68437
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A;Title: Cloning and expression of a gene encoding an interleukin 3 receptor-lik A; Reference number: A35782; MUID:90319131
A; Accession: A35782
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C;Keywords: alternative splicing; appetite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U49106; NID:g1195484; PIDN:AAC52420.1; PID:g1195485 A;Experimental source: splice form Ra; tissue hypothalamus A;Note: the nucleotide sequence was submitted to the EMBL Data Library, February C;Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439,
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                                                                                                                                                                           F;464-896/Domain:
                                                   Query Match
Best Local S
Matches 49
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Matches
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les 57; Conser
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DLVCYTDYLQTVICILEMWN---
                                                   l Similarity
49; Conserv
                                                12.1%;
llarity 22.6%;
Conservative 4
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                                                                                                                                                                      cytokine receptor homology <CRS2> transmembrane #status predicted <TMM> intracellular #status predicted <INT>
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31.1%;
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; Pred. No. 0.0001;
22; Mismatches 6
                                                Score 144; DB
Pred. No. 0.00
11; Mismatches
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  -LHPSTLTLTWQDQYEELKDEATSCSLHRS 51
                                                                                                   DB 1;
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S68440
                                                                                                                                                                       leptin receptor, splice form Ob-Rb - mouse
C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1998 #sequence_revision 31-Dec-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: tissue hypothalamus
A; Note: the nucleotide sequence was submitted to the EMBL Data Library,
C; Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PI
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C;Species: Mus musculus (house mouse)
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 31-Dec-2000
                                         A;Title: Abnormal splicing of the leptin receptor in diabetic mice A;Reference number: S68437; MUID:96231997
A;Accession: S68438
                                                                                                           C; Accession: S68438; S68441
R; Lee, G.H.; Proenca, R.; M
Nature 379, 632-635, 1996
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                      A; Status: nucleic
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A; Residues: 1-900 <LEE>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            354
                                                                                                                                                                                                                                                                                                                                   327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYLENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 QLEPDTSYCARVRVKPI -- SNYDGIWSKWSEEYTWKT 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    300
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                                                                                                                                                                                                                                                                                                                                                                          205 QTQ
                                                                                                                                                                                                                                                                                                                                                                                                                      277 T--IVREAAEIVSATSLLVDSVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         V Match 12.1%; Score 144; DB 2; Local Similarity 31.1%; Pred. No. 0.00011;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88 QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           39 LKDE----ATSCSLHRSAHNATHATYTCHMDVFH-----FMADDIFSVNITDQSGNYS
                                                                                                                                                                                                                                                                                                                                   OLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPWAYSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKDSFQTVQCNCSLRGC-----ECHVPVPRAKLNYALLMYLEITSAGVSFQSPLMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-RDSYSLHWETQKMAYSFI----EHTFQVQYKKKSDSWEDSKTENLDRAHSMDLS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PGASVYTRYHCSLPVPEPSAHSQYTVSVK------HLEQGKFIMSYNHIQMEPPTLNLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AHNATHATYTCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLA-ESIKPAPP-FNVTV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLQCFFDGIQSLHCSWEVWTQTTGSVSFGLFYRPSPVA---
type: mRNA
                                                                                                                                                                                                                                                                                                                                   329
                                                                                                                                                                                                                                                                                                                                                                               207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                      acid
                      sequence not shown
                                                                                                                                  Montez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                  J.M.; Carroll,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                      -GSSYEVQVRSKRLDGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206
                                                                                                                                  K.M.; Darvishzadeh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    K.M.; Darvishzadeh,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diabetic mice
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                                                                                                                                                                                                                                                                                                                                                                                                                        -GVWSDWSSPQVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
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PIR:S68439,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.G.;
                                                                                                                                  J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145
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                                                                                                                                  Lee,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11;
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J.I.;

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A; Residues: 664-1162 <LEE1>
A; Cross-references: EMBL:U49107; NID:gl195486; PIDN:AAC52421.1; PID:gl195487
A; Cross-references: EMBL:U49107; NID:gl195486; PIDN:AAC52421.1; PID:gl195487
A; Kote: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
A; Note: only a part of the translation is shown
A; Accession: S68441
A; Status: nucleic acid sequence not shown; translation not shown
A; Residues: 1-796, GMCTVIFMD < CLEE2>
A; Cross-references: EMBLVIFMD / NID:gl195492; PIDN:AAC52424.1; PID:gl195493
A; Experimental source: Splice form Re; tissue hypothalamus
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1996
A; Note: this sequence from splice form Re is included to produce a complete sequence
C; Comment: For alternative splice forms, see PIR:S68437, PIR:S68438, PIR:S68439, PIR:S
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A;Residues: 1-539 <KON>
A;Cross-references: GB:MZ8052; NID:g198313; PIDN:AAA39283.1;
C;Superfamily: fibronectin type III repeat homology
C;Keywords: cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kono, T.; Doi, T.; Yamada, G.; Hatakeyama, M.; Minamoto, S.; Tsudo, M.; Miyasaka, M.; Proc. Natl. Acad. Sci. U.S.A. 87, 1806-1810, 1990
A;Title: Murine interleukin 2 receptor beta chain: dysregulated gene expression in lymple efference number: A35052; MUID:90175385
Cccession: A35052
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interleukin-2 receptor beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text_change 05-Nov-1999
C;Accession: A35052
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
atches 57
                            101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177 LKDSFQTVQCNCSLRGC-----ECHVPVPRAKLNYALLMYLEITSAGVSFQSPLMS 227
                                                                                                                          61
                                                                                                                                                                           31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88
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                                                                                                                                                                           CSHLECFYNSRANVSC - - - MWS - HEEALNV - - -
                                                                                                                                                                                                                      CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
                                                                       TCELTLVRQASWACNLILGSFPESQSLTSVDLLDINVVCWEEKGWRRVKTCDFHPFDNLR 132
                                                                                                                          TCHMDVFH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTQ 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T--IVREAAEIVSATSLLVDSVLP----GSSYEVQVRSKRLDGS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DPWAVSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIF 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QECGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LQ--PMLV---VKPDPPLGLHMEVTDDGNLKISWDSQTMAPF-----PLQYQVKYLENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 57;
                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                             11.8%;
                                                                                                                                                                                                                                                                         43;
                                                                                                                     ----FMADDIFSVNIT--DQSGNYSQECGSFLLAESIK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22;
                                                                                                                                                                                                                                                                       Score 141.5; DB 2
Pred. No. 9.1e-05;
3; Mismatches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 144;
Pred. No. 0.
SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRR 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                         96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
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C;Accession: A45266 R;Vigon, I.; Mornon, J.P.; Cocault, L.; Mitjavila, M.T.; Tambourin, P.; Gisselbrecht, Proc. Natl. Acad. Sci. U.S.A. 89, 5640-5644, 1992 A;Title: Molecular cloning and characterization of MPL, the human homolog of the v-mp A;Reference number: A45266; MUID:92302297
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MPL-K protein precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
C;Accession: B45266
C;Accession: B45266
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                                                                                                                                                                                                  C; Keywords: transmembrane protein
                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-635 < VIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 05-Nov-1999
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MPL-P protein precursor - human
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A; Residues: 1-579 < VIG>
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                                                                                                                                                                                                                         A;Cross-references: GB:M90102; NID:g184260; PIDN:AAA69971.1; PID:g184261
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                                                                                                                                                                                                                                                                                                  A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         384 WIHQAVRLPTPNLHWREISSGHLELEW----QHPSSWAAQ-ETCYQLRYTGEGHQDWKV- 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      330 IWENCEEEEKTNPGLQTPQFSRCHFKSRNDSIIHIL-----VEVTTAPGTVHSYLGSPF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94
4 LVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSL--HRSAHNATHATY- 60 | | : | | : | | | | | | | |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 LVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSL--HRSAHNATHATY- 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLAESIK-PAPPFNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRG-DPWAVS 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRRKLISVDSRSVSLLP-----LEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVI 203
                                                                           Similarity 59; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LEPPLGARGGTLELRPRSRYRLQLRA-RLNGPTYQGPWSSWSDPTR 482
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24.0%;
                                                                                                  11.6%;
24.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25;
                                                                           25;
                                                                      Score 139; DB 2;
Pred. No. 0.00019;
25; Mismatches 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 139; DB 2; Pred. No. 0.00017;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --- DHASSQGFFYHSRARCCPRDRYP 329
                                                                           Indels
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                                                                           ; 88
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                                                                           Gaps
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                                                                           14;
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leptin receptor, Ob-Rb - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 01-Dec-2000
C;Accession: JC4895; JC4896; JC4897; PC4184; JC4797
R;Takaya, K; Ogawa, Y; Isse, N; Okazaki, T; Satoh, N; Masuzaki, H; Mori, Biochem. Biophys. Res. Commun. 225, 75-83, 1996
A;Title: Molecular cloning of rat leptin receptor isoform complementary DNAs-id A; Reference number: JC4895; MUID:96332408
A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-Jan-1998 #sequence_revision 13-Feb-1998 #text_change 05-Nov-1999
C;Accession: S74225
R;Wang, M.Y.; Zhou, Y.T.; Newgard, C.B.; Unger, R.H.
FEBS Lett. 392, 87-90, 1996
A;Title: A novel leptin receptor isoform in rat.
A;Reference number: S74225; MUID:96368027
A;Accession: S74225; MUID:96368027
                                                                                                                                                                                                                                                              Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: rOb-R
C;Keywords: appet
F;840-860/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-895 <WAND
A;Cross-references: EMBL:U53144; NID:g1395212; PIDN:AAB03088.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qγ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Best Local
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                                                                                                                                                                                                                                                                                                         -IVREAAEIVSDTSLLVDSVLP-----GSSYEVQVRSKRLDGS---GVWSDWSLPQLFTT
                                                                                                                                                                                                                                                                                                                                                                                             CGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDP
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                                                                                                                                                                                                                                                                                                                                       WAVSPRRKLISVDSRSV-SLLPLEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVIFQT
                                                                                                                                                                                                                                                                                                                                                                        --PMLV---VKPDPPLGLRMEVTDDGNLKISWDSQTKAPF-----PLQYQVKYLENST-
                                                                                                                                                                                                                                                                                                                                                                                                                                            LKDSFQTVQC------NCSVRECECHVPVPRAKVNYALLMYLEITSAGVSFQSPLMSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRRKLISVDSRSVSLLP------LEFRKDSSYELQVRAGPMPGSSYQGTWSEWSDPVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           appetite; transmembrane protein omain: transmembrane #status pred
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 138; DB
Pred. No. 0.00
23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                   complementary DNAs-identifica
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                                                                                  K.; Tamu
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interleukin-4 receptor precursor - human

N;Alternate names: IL-4 receptor

C;Species: Homo sapiens (man)

C;Cate: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999

C;Accession: A60386; A47603

R;Galizzi, J.P.; Zuber, C.E.; Harada, N.; Gorman, D.M.; Djossou, O.; Kastele Int. Immunol. 2, 669-675, 1990

A;Title: Molecular cloning of a cDNA encoding the human interleukin 4 recept A;Reference number: A60386; MUID:91120547

A;Accession: A60386

A;Status: not compared with conceptual translation

A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA A;Rosidues: 1-889, 'RADTL' <II2> A;Cross-references: DBJ:D84125; NID:g1374707; PIDN:BAA12230.1; PID:g1374708 A;Experimental source: adipose cell C;Comment: This receptor is obese-phenotype-linked mutant, found in the Zuck
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 840-1162 <IID>
A;Cross-references: DDBJ:D84550
R;Iida, M.; Murakami, T.; Ishida, K.; Mizuno, A.; Kuwajima, M.; Shima, Biophys. Res. Commun. 222, 19-26, 1996
A;Title: Phenotype-linked amino acid alteration in leptin receptor cDN A;Reference number: JC4797; MUID:96212906
A;Accession: JC4797
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A;Title: Substitution at codon 269 (glutamine-proline) of the leptin receptor (OB-R) A;Reference number: PC4184; MUID:96295531
A;Accession: PC4184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-796, 'G', 1157-1158, 'TVLLLN'
A; Cross-references: DDBJ: D85559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Keywords: appetite; transmembrane protein F;840-860/Domain: transmembrane #status predicted F;861-1162/Domain: intracellular #status predicted
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A; Residues: 1-889, 'RADTL'
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A; Residues: 1-1162 <TAK>
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A;Cross-references: DDBJ:D85557
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Best Local S
Matches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207 Q 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -IVREAAEIVSDTSLLVDSVLP-----GSSYEVQVRSKRLDGS---GVWSDWSLPQLFTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGSFLLAESIKPAPP--FNVTVTFSGQYNISWRSDYEDPAFYMLKGKLQYELQYRNRGDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --PMLV---VKPDPPLGLRMEVTDDGNLKISWDSQTKAPF-----PLQYQVKYLENST-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKDSFQTVQC----
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56; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 138; Ub 2, No. 0.0005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in leptin receptor cDNA from zucker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
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                                                                                                                                                                                    O.; Kastelein,
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C;Genetics:
A;Genetics:
C;Keywords:
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C;Ceytokine receptor;
A;Ge-Signal sequence #status predicted <SIG>
F;1-25/Domain:
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R;Idzerda, R.L.; March, C.J.; Mosley, B.; Lyman, S.D.; Vanden Bos, T.; Gimpel, S.D.; D.
J. Exp. Med. 171, 861-873, 1990
A;Title: Human interleukin 4 receptor confers biological responsiveness and defines a A;Reference number: A47603; MUID:90171849
A;Recession: A47603
A;Molecule type: mRNA
A;Residues: 1-74,'I',76-825 <IDZ>
A;Cross-references: GB:X52425; NID:933833; PIDN:CAA36672.1; PID:933834
                                                                                                                                                                                                                                                                                                                                                                A;Note: sequence inconsistent with the nucleotide translation A;Note: sequence extracted from NCBI backbone (NCBIN:60818, NCBIP:60819) C;Superfamily: fibronectin type III repeat homology C;Keywords: cytokine receptor
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A;Molecule type: mRNA
A;Residues: 1-537 <PAG>
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Eur. J. Immunol. 21, 213:-2138, 1991
Eyr. J. Immunol. 21, 213:-2138, 1991
A;Title: Molecular cloning of cDNAs for the rat interleukin 2 receptor alpha A; Reference number: A46535; MUID:91364784
A; Accession: B46535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        134 NVSDTLLLTWSNPY -- PPDNYLYNHLTYAVNIWSENDP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      85 VCHL-----LMDDVVSAD-----NYTLDLWAGQQLLWKGSFKPSEHVKPRAPGNLTVHT 133
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                                                                               1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEA---TSCSLHRSAH---- 53
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    CSHLKCFYNSRANVSC---MWS-----
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                                                                                                                                                          11.2%; Score 134; DB 2;
23.1%; Pred. No. 0.00042;
tive 41; Mismatches 72;
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    -----PEEALNVTSCHIHAKSDMRHW 70
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                                                           RRRLLDRSWEDASVFSLKQRQQWIFLETLTPDTSYELQVRVIAQRGKT--RTWSPWSQPM
                                                                                                                                             IKPAPPFNVTVTF--SGQYNISWR----SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSP 152
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Search completed: June 28, 2002, 07:42:53 Job time: 128 sec

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ALIGNMENTS	AAY92208	AAV92207	AAB19807	AAW24973	AAW09822	AAW09821	AAW36616	AAB29747	AAY72135	AAY95295	AAW35294	AAW36614	AAU69134	AAB29748	AAY72136	AAG63812	AAY95296	AAW33603	AAW41502	AAW41520	AAW36613	AAW35295	AAW24972	AAW56260	AAW56261	AAU69135	AAU69136	AAU69137	AAU69139	AAU69140	AAU69141	13	AAG00283
	IL-13/IL-4 dual tr	TIL-A dual		Human interleukin-		Mouse interleukin-	us maca		interleuki	inding) IL-13	Ľ	Canine interleukin			acid sequen	3 binding	ß	Human cytokine/pep				Human interleukin-	⊏							н	e IL-13Ral	Human secreted pro

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RESULT
AAR47149
  Asao H, E
Suzuki M,
                WPI; 1994-017546/03.
N-PSDB; AAQ54829.
                                                                                                                                                                              Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator;
rheumatoid arthritis; transplant rejection; primer;
polymerase chain reaction; PCR; amplification.
DNA and protein sequences of IL-2 gamma chain
                                                                                                                                             EP578932-A.
                                                                                                                                                                                                                                                   AAR47149;
                                                                   (AJIN ) AJINOMOTO KK. (SUGA/) SUGAMURA K.
                                                                                            23-APR-1992;
                                                                                                            22-APR-1993;
                                                                                                                              19-JAN-1994.
                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                 IL-2 receptor gamma chain.
                                                                                                                                                                                                                                13-JUN-1994 (first entry)
                                                                                                                                                                                                                                                                   AAR47149 standard; Protein;
                                         Hamuro J, I
                                                                                            92JP-0104947
                                                                                                            93EP-0106561
                                         Nakamura
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                                                  Shimamura
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    useful

                                                 Sugamura
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immune
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RESULT
AAR47148
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Best Local Similarity
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Asao H,
Suzuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The human IL-2 receptor gamma chain preform (AAR47148), including the signal peptide, is encoded by the sequence given in AAQ54828. The mature protein (AAR47149) is encoded by sequence AAQ54829. A soluble form of IL-2 receptor gamma chain (AAR47150) is encoded by AAQ54830, while a soluble form suitable for expression in prokaryotes (AAR47151) is encoded by AAQ54831. Primers 1-6 (AAQ54820-25) are based on the N-terminal sequence of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma chain receptor cDNA. Primers AAQ54826-27 are used to obtain the protein given in AAR47151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 41; 50pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           regulatory agents for treatment of e.g. rheumatoid arthritis and transplant rejection
                                                                                                                                                                                    19-JAN-1994
                                                                                                                                                                                                                        EP578932-A
                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                  Interleukin-2 receptor gamma chain; IL-2; receptor; rheumatoid arthritis; transplant rejection; primer; polymerase chain reaction; amplification; ss.
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                                                                                                            23-APR-1992;
                                                                                                                                                 22-APR-1993;
                                                                                                                                                                                                                                                                           Peptide
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                                                      (SUGA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DYRHKESLPSVDGQKRYTERVRSRENPLCGSAQHWSEWSHPIHWGSNTSKEN 232
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                                                      AJINOMOTO KK.
SUGAMURA K.
                     Hamuro J, Nakamura M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
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 Takeshita T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma chain.
                                                                                                            92JP-0104947
                                                                                                                                                 93EP-0106561
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1..22
/label= Sig_peptide
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Pred. No. 6.7e-116;
; Mismatches 0;
                     Shimamura
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                   Sugamura
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RESULT
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19-MAY-1999;
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DB; AAQ54828.
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                                                                                                         Yancopoulos GD
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99US-0313942
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                  IL-4 trap; cytokine; antagonist; CNTF; receptor; fusion protein; cytostatic; immunomodulator; osteopathic.
                                                                                  Fusion polypeptide 424, IL-4 trap.
                                                                                                                             01-AUG-2000
                                                                                                                                                                         AAY92201
                                                                                                                                                                                                               AAY92201 standard; Protein; 694 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disorders such as osteoporosis and primary and secondary effects of cancer including multiple myeloma or cachexia.
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                                                                                                                                                                                                                                                                                                                      181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                             143
                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDDREPRRQA 120
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mes 232; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 60
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                                                                                                                                                                                                                                                                                                                                                                                                         tqmlklqnlvipwapenltlhklsesqlelnwnnrflnhclehlvqyrtdwdhswteqsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOMLKLONLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tnltlhywyknsdndkvqkcshylfseeitsgcqlqkkeihlyqtfvvqlqdpreprrqa 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inttiltpngnedttadfflttmptdslsvstlplpevqcfvfnveymnctwnsssepqp 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           691 AA;
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                                                                                                                             (first entry)
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181

DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN

TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180

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tqmlklqnlvipwapenltlhklsesqlelnwnnrflnhclehlvqyrtdwdhswteqsv

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Best Local Similarity
Matches 232; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention concerns production of antagonists to any cytokine that utilizes an alpha specificity determining component, which when combined with the cytokine, binds to a first beta signal transducing component to form a non-functional intermediate which then binds to a second beta
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19-MAY-1999;
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                                                                                                                                                                                                                                                                   Sequence
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83
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                                                                            TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
tnltlhywyknsdndkvqkcshylfseeitsgcqlqkkeihlyqtfvvqlqdpreprrqa 142
                                                                                                                                                                                                                                                                   694 AA;
                                                                                                                                                             100.0%; score 1288; DB:
ilarity 100.0%; Pred. No. 1.8e-1:
Conservative 0; Mismatches
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The invertion concerns production of antagonists to any cytokine that cutilizes an alpha specificity determining component, which when combined CC with the cytokine, binds to a first beta signal transducing component to signal transducing component causing beta receptor dimerization, the soluble alpha specificity determining component of the receptor (sR-alpha) and the extracellular domain of the first beta signal transducing component of the cytokine receptor (beta-1) are combined to CC transducing component of the cytokine receptor (beta-1) are combined to CC form heterodimers (sR-alpha:beta-1) that act as antagonist to the CC cytokine by binding the cytokine receptor (beta-1) are combined to CC receptor components are shared by cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines such as the CNTF (ciliary neurotrophic factor) family of cytokines. The invention provides the basis for the development of IL-6 antagonists, as they show that if, in CC component, can be formed, it will effectively block the action of the ligand, its alpha recepotr and its beta-1 receptor CC component, can be formed, it will effectively block the action of the CC of the extracellular domains of the alpha specificity determining CC components of their receptors and the extracellular domain of gpl30.

The resultant heterodimers, function as high-affinity traps, rendering CC native membrane-bound forms of their receptor. The nurleic acids and complex with the component contents and the extracellular domain of gpl30.
                                                        native membrane-bound forms of their receptor. The nucleic acids and polypeptides are useful for treating cytokine-related diseases or disorders such as osteoporosis and primary and secondary effects of
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19-MAY-1999;
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DB; AAA09045.
                                        including multiple myeloma
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99US-0313942
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                                        or cachexia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytokine receptor; gamma common chain; gc chain; human; blocking agent; monoclonal antibody; CP.B8; immunological disease;, myssthenia gravis; rheumatoid arthritis; lupus; multiple sclerosis; insulin-dependent diabetes; inflammatory bowel disease; sympathetic ophthalmia; uveitis; allergy; asthma; infection;, graft versus host disease; psoriasis; immunosuppressive; therapy.
This polypeptide comprises a fusion between the N-terminal 254 amino acids of the human mature cytokine receptor gamma common
                                                        Blocking agents of the gamma common particularly monoclonal antibodies, treatment of immunological diseases
                                                                                                           WPI; 1998-008885/01
N-PSDB; AAT97439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW31646;
                                   Example 1; Page 79-80; 111pp; English.
                                                                                                                                                Benjamin CD,
                                                                                                                                                                                                                        09-MAY-1997;
                                                                                                                                                                                                                                                 20-NOV-1997.
                                                                                                                                                                                                                                                                                                          Domain
                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human cytokine receptor gc chain-Ig fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW31646 standard; Protein;
                                                                                                                                                                      (BIOJ ) BIOGEN INC.
                                                                                                                                                                                                10-MAY-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dyrhkfslpsvdgqkrytfrvrsrfnplcgsaqhwsewshpihwgsntsken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tnltlhywyknsdndkvqkcshylfseeitsgcqlqkkeihlyqtfvvqlqdpreprrqa
                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                Burkly
                                                                                                                                                                                               96US-0017466
                                                                                                                                                                                                                        97WO-US07870
                                                                                                                                                                                                                                                                                                        /note= "IgG1 hinge region" 264..482
                                                                                                                                                                                                                                                                                                                                                        /note= "gc chain N-terminal region"
255..482
                                                                                                                                                                                                                                                                                                                                  255..264
                                                                                                                                                                                                                                                                                                                                            /note= "IgG1 constant region"
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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15
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                                                                                                                                                                                                                                                                                               "IgG1 CH2 and CH3 constant domains1"
                                                                                                                                                Hession C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   482
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                                                                                                                                                Whitty A;
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                                                                        induce T cell anergy for
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RESULT
AARA/7151
ID AARA
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Best Local S
Matches 231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interleukin-2 receptor gamma chain; IL-2; receptor; immunoregulator;
rheumatoid arthritis; transplant rejection; primer;
polymerase chain reaction; PCR; amplification.
DNA and protein sequences of IL-2 gamma chain - useful as immune regulatory agents for treatment of e.g. rheumatoid arthritis and transplant rejection % \left( 1\right) =\left( 1\right) +\left( 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR47151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-APR-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IL-2 receptor gamma chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR47151 standard; Protein; 230
                                                                                                                                                                         N-PSDB; AAQ54831.
                                                                                                                                                                                                                                                                                                     Suzuki M,
                                                                                                                                                                                                                                                                                                                                             Asao
                                                                                                                                                                                                                                                                                                                                                                                                                         (SUGA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        203
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                                                                                                                                                                                                                                                                                                                                                                                                                         SUGAMURA K.
                                                                                                                                                                                                                                                                                                 Hamuro J, Nakamura
d, Takeshita T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AJINOMOTO KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            482 AA;
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Pred. No. 4e-115;
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                                                                                                                                                                                                                                                                                                                                    Sugamura
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Best Local
                                Asao H, H
Suzuki M,
                                                                                                                                                                                                            Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  terminal sequence of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma chain receptor cDNA. Primers AAQ54826-27 are used to obtain the protein given in AAR47151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The human II-2 receptor gamma chain preform (AAR47148), including the signal peptide, is encoded by the sequence given in AAQ54828. The mature protein (AAR47149) is encoded by sequence AAQ54829. A soluble form of II-2 receptor gamma chain (AAR47150) is encoded by AAQ54830, while a soluble form suitable for expression in prokaryotes (AAR47151) is encoded by AAQ54831. Primers 1-6 (AAQ54820-25) are based on the N-
                                                                                                                                                                                                                                                                    Interleukin-2 receptor gamma chain; IL-2; receptor; rheumatoid arthritis; transplant rejection; primer; polymerase chain reaction; PCR; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 22-23, 35-36; 50pp; English
N-PSDB; AAQ54830
           WPI; 1994-017546/03
                                                                                                                                                                                                                                                                                                                                            13-JUN-1994
                                                                                                                                                                                                                                                                                                                                                                                       AAR47150 standard;
                                                                  (AJIN ) AJINOMOTO KK.
(SUGA/) SUGAMURA K.
                                                                                                      23-APR-1992;
                                                                                                                              22-APR-1993;
                                                                                                                                                    19-JAN-1994
                                                                                                                                                                           EP578932-A.
                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                   IL-2 receptor gamma chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt lnttiltpngnedttadfflttmptdslsvstlplpevqcfvfnveymnctwnsssepqp}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      230;
                                Hamuro J, l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               230 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.1%; Score 1277; DB 15; ilarity 100.0%; Pred. No. 4.4e-115 Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                      92JP-0104947
                                                                                                                              93EP-0106561
                                                                                                                                                                                               /label= Sig_peptide
                                                                                                                                                                                                              Location/Qualifiers
1..22
                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                             Nakamura M,
                                                                                                                                                                                                                                                                                                                                                                                          252
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                                             Shimamura
                                             Ţ
                                             Sugamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                              immunoregulator;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The human IL-2 receptor gamma chain preform (AAR47148), including the signal peptide, is encoded by the sequence given in AAQ54828. The mature protein (AAR47149) is encoded by sequence AAQ54829. A soluble form of IL-2 receptor gamma chain (AAR47150) is encoded by AAQ54830, while a soluble form suitable for expression in prokaryotes (AAR47151) is encoded by AAQ54831. Primers I-6 (AAQ54820-25) are based on the N-terminal sequence of IL-2 receptor gamma chain, and are used to isolate IL2 receptor gamma chain receptor DNA. Primers AAQ54826-27 are used to obtain the protein given in AAR47151.
                                                                                                                                                                                                                                                                   Interleukin-4; IL-4; gamma chain component; immunosuppressants; anti-allergy agent; signal transmission inhibitor; autoimmune; disease; anti-inflammatories; anaphylactic shock; bronchial asthma; interleukin-2; IL-2; atopic dermatitis; urticaria.
                                                                                                                                                  07-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                              26-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                             AAR82934;
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR82934 standard; Protein; 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA and protein sequences of IL-2 (regulatory agents for treatment of transplant rejection
                                             WPI; 1995-243601/32
                                                                       (AJIN ) AJINOMOTO KK. (SUGA/) SUGAMURA K.
                                                                                                                        08-SEP-1993;
                                                                                                                                                                                  13-JUN-1995
                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 21-22,
Novel interleukin-4 receptor monoclonal antibodies inhibit signal
                              N-PSDB; AAT04952
                                                                                                                                                                                                                                                                                                                                               Interleukin 4 component common to the IL-2 receptor gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tqmlklqnlvipwapenltlhklsesqlelnwnnrflnhclehlvqyrtdwdhswteqsv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tnltlhywyknsdndkvqkcshylfseeitsgcqlqkkeihlyqtfvvqlqdpreprrqa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               252 AA;
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                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                      93JP-0223574
                                                                                                                                                   94JP-0213706
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                                               New nucleic acid molecule encoding a human cytokine receptor common gamma chain like polypeptide, useful for treating, preventing and/o diagnosing e.g. tumors, inflammatory diseases and immunodeficiency
                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                             tumours; infections; inflammatory; immune disorder;
neurodegenerative; cardiovascular; disorder.
                                                                                                                                                                                                                                                                                                                                                                Bos taurus interleukin-2 receptor gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transmission - useful as immunosuppressants and anti-allergy agents.
                                                                                                                               Ruben
                                                                                                                                                       (HUMA-) HUMAN GENOME
                                                                                                                                                                                18-AUG-1999;
                                                                                                                                                                                                        17-AUG-2000;
                                                                                                                                                                                                                                   22-FEB-2001
                                                                                                                                                                                                                                                            WO200112672-A2
                                                                                                                                                                                                                                                                                     Bos taurus
                                                                                                                                                                                                                                                                                                                                        Cytokine receptor common gamma chain like;
                                                                                                                                                                                                                                                                                                                                                                                          10-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                     AAB71682;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB71682 standard; protein; 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            atopic dermatitis and urticaria
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                                                                                                     2001-147547/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dyrhkfslpsvdgqkrytfrvrsrfnplcgsaqhwsewshpihwgsnts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTS 229
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           Fig
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                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                99US-0376430
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            2
           288pp; English
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                                                                                                                                                        SCI INC
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Pred. No. 1.3e-114;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                         CRCGCL; human;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a human cytokine receptor common gamma chain like protein (CRCGL). The invention is useful for treating, preventing and/or diagnosing conditions such as tumours, infections, inflammatory diseases, immune disorders, neurodegenerative disorder and cardiovascular immune disorders, neurodegenerative disorder and cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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12-MAR-1993;
                                           10-MAR-1994;
                                                                                 15-SEP-1994
                                                                                                                                                                                            Modified-site
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93US-0031143
                                        94WO-US02891
                                                                                                                                                                                                                                                                           84..86
/label=
96..98
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Coresponding codon CAG"
71..73
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "transmembrane domain"
331
                                                                                                                                                                                                                                  /label= N-glycosylation_site 159..161
                                                                                                                                                                                                                                                                                                                                                                 /label= N-glycosylation_site
75...77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note= "signal peptide" 258..284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                /label=
                                                                                                                                                                                                                                                                                                                                        /label= N-glycosylation_site
                                                                                                                                                                                                                                                                                                l= N-glycosylation_site
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AAG00283
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Best Local S
Matches 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAQ71977 is the DNA sequence of murine IL-2R gamma AAR59094, this was used in the development of a claimed method for the diagnosis of X-linked severe combined immunodeficiency (XSCID), in female carriers and male sufferers.
WPI; 2000-500381/45
N-PSDB; AAC00289.
                                                                                                                                                                                                                                                        Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        comprises detecting mutated IL-2R gamma gene, also vectors and transgenic animals containing the mutated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Diagnosis of X-linked severe combined immunodeficiency (XSCID)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1994-303046/37.
N-PSDB; AAQ71977.
                                          Dumas Milne Edwards J,
                                                                                                         26-FEB-1999;
                                                                                                                                      21-FEB-2000; 2000EP-0200610
                                                                                                                                                                      06-SEP-2000
                                                                                                                                                                                                 EP1033401-A2
                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                           Human secreted protein,
                                                                                                                                                                                                                                                                                                                                            06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                            AAG00283;
                                                                                                                                                                                                                                                                                                                                                                                                          AAG00283 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1993;
                                                                        (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQAT 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nltlhyrykvsdnntfqecshylfskeitsgcqiqkediqlyqtfvvqlqdpqkpqrrav 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt sskvlmssanedikadliltstapehlsaptlplpevqcfvfnieymnctwnsssepqat}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qklnlqnlviprapenltlsnlsesqlelrwksrhikerclqylvqyrsnrdrswteliv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΨJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   369 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                         99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66.3%; Score 854.5; DB 15; 67.2%; Pred. No. 5e-74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO,
                                                                                                                                                                                                                                                                                                            SEQ ID
                                          Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Noguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                              4364
                                              Giordano
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RESULT 1
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
Novel isolated canine protein, preferably canine immunoglobulin G protein or canine interleukin-13 receptor protein useful for regulating immune response of an animal and for developing regulatory compounds -
                                                                                                                                                                                                  07-APR-2000;
07-APR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a polypeptide encoded by one of a of 5' ESTs derived from mRNAs encoding secreted proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                         N-PSDB;
                                                                                                                                                                                                                                                         09-APR-2001; 2001WO-US11498
                                                                                                                                                                                                                                                                                                                               WO200177332-A2
                                                                                                                                                                                                                                                                                                                                                                 Canis familiaris.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-3523 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU69138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
                                                                                                                            McCall CA,
                                                                                                                                                                (HESK-) HESKA CORP
                                                                                                                                                                                                                                                                                           18-OCT-2001
                                                                                                                                                                                                                                                                                                                                                                                                                    IL-13Ralpha1; IR-13Ralpha2;
immunoglobulin light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAU69138 standard;
                                                                                                                                                                                                                                                                                                                                                                                                       immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKE 99
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                                                                     2001-657172/75
DB; AAS59970.
                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-13 receptor alphal; interleukin-13 receptor 3Ralphal; IR-13Ralpha2; Immunoglobulin heavy chain; IgG F noglobulin light chain; lambda; immunosuppressive; gene t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tnltlhywyknsdndkvqkcshylfseeitsgcqlqkke 121
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                                                                                                                                                                                                                                                                                                                                                                                                   response.
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                                                                                                                          Tang L;
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                                                                                                                                                                                                  2000US-195659P.
2000US-195874P.
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100.0%;
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Pred. No. 1.5e-44;
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The 5' ESTs
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                                          07-APR-2000;
07-APR-2000;
                                                                                         09-APR-2001; 2001WO-US11498
                                                                                                                                                    WO200177332-A2
                                                                                                                                                                                                                             Dog; interleukin-13 receptor alpha1; interleukin-13 receptor alpha2; IL-13Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG FC; immunoglobulin light chain; lambda; immunosuppressive; gene therapy;
                                                                                                                                                                                                                                                                                             Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-B9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention concerns an isolated canine protein, preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 46; Page 191-193; 221pp; English
                                                                                                                          18-OCT-2001.
                                                                                                                                                                                     Canis familiaris
                                                                                                                                                                                                                                                                                                                              29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                          AAU69141 standard; Protein; 561
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPRE--PRR 118
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             HESKA CORP
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Pred. No. 4.7e-12;
7; Mismatches 103
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RESULT 15
AAU69140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 46; Page 210-212; 221pp; English.
                                                                                                                     Canis familiaris
                                                                                                                                                                                                                                                                                                                             Canine IL-13Ralpha2/IgG-Fc fusion protein PcaIL-13Ralpha2-Fc-B9 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAU69140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU69140 standard; Protein;
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18-OCT-2001
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                                                                                                                                                                                                                                 interleukin-13 receptor alpha1; interleukin-13 receptor 3Ralpha1; IR-13Ralpha2; Immunoglobulin heavy chain; IgG I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psyfifqlqnivkpmppdylsltvknseeinlkwnmpkgpipakcfiyeiefted-gttw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2001-657172/75.
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                                                                                                                                                                              response.
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26.1%;
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Best Local Similarity 26.1
Matches 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        raised against them, fusion proteins between the IgG and IL-13R proteins and methods of isolating regulators of them. The regulators are useful for regulating an immune response in a canine. The proteins useful to develop regulatory compounds including inhibitors and activators that, when administered to a canine in an effective manner, are capable of protecting canine from disease mediated by IL-13Ralpha or IL-13. The regulators are useful for treating canine IgG (heavy and/or light chain) and/or canine IL-13R mediated responses. The molecules of the invention are useful to regulate the immune response of an animal (e.g. by gene therapy). The present sequence represents a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention concerns an isolated canine protein, preferably canine immunoglobulin G (IgG) protein or canine interleukin-13 (IL-13) receptor protein, the nucleic acids encoding them, antibodies
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07-APR-2000;
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                                                                                                                                                                                          QATQMLKLQNLVIPWAPENLTLHKLSESQLELNWN---NRFLNHCLEHLVQYRTDWDHSW 175
                                                                                                                                              psyfifqlqnivkpmppdylsltvknseeinlkwnmpkgpipakcfiyeiefted-gttw
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DB; AAS59974.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 AA;
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2000US-195874P.
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GMCR_HUMAN
PRIR_COLLI
IL4R_MOUSE
PRIR_MOUSE
PRIR_COLLI
IL5R_MOUSE
PRIR_CEREL
IL5R_HUMAN
IL5B_HUMAN
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IL5B_HUMAN
IL5B_MOUSE
PRIR_RAT
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                      VARIANT XSCID GLN-237 G-H-W INS.
MEDLINE-95164726; PubMed=7860773;
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gamma-chain mutation causing X-linked
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MEDLINE-96013903; PubMed-7557965;
MEDLINE-96013903; PubMed-7557965;
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severe combined immunodeficiency disea
high-affinity IL-2 receptor binding.";
Eur. J. Immunol. 24:475-479(1994).
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"Impairment of ligand binding and growth signaling of mutant IL-2 receptor gamma-chains in patients with X-linked severe combined immunodeficiency."
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Noguchi M., Nakamı
Leonard W.J.;
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"Detection of three nonsense mutations
"Detection of three programma chain
the interleukin-2 receptor gamma chain
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J. Clin. Invest.
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VARIANT XSCID GLN-293.

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MEDLINE-95190013; PubMed-7883965;

MEDLINE-95190013; PubMed-7883965;

Schmalstieg F.C., Leonard W.J., Noguchi M., Berg M., Ruc Schmalstieg F.C., Leonard W.J., Noguchi M., Ruc Denney R.M., Dave S.K., Brooks E.G., Goldman A.S.;

"Missense mutation in exon 7 of the common gamma chain moderate form of X-linked combined immunodeficiency.";

"Olin. Invest. 95:1169-1173(1995).
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entities
or send a
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1. SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 AND PROBABLY ALSO THE IL-13 RECEPTORS.

1. SUBCELLULAR LOCATION: Type I membrane protein.

1. DISEASE: DEFECTS IN ILLEG ARE THE CAUSE OF A SEVERE COMBINED IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINENIA, SWISS TY OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (XSCID).

1. SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

1. SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.

1. DATABASE: NAME-PROW, NOTE-CD guide CD132 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd132.htm".

1. DATABASE: NAME-PROW, NOTE-CD guide CD132 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd132.htm".
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J. Clin. Inve
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Sharfe N., Shahar M., Roifman C.M.;
"An interleukin-2 receptor gamma chain
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RESULT 2
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DT 01-FEB
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DE (Inter
GN ILZRG;
OS Canis
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01-FEB-1995 (Rel. 31, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Cytokine receptor common gamma chain precursor (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL-2R gamma chain)
                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Spleen;
MEDLINE=95130114; PubMed=7829104;
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Canis familiaris (Dog).
Finharyota: Metazoa; Chordata;
                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 23:69-74(1994)
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                                                         InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003531; Hematopo_receptor_S_F1.
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
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                               PROSITE; PS01355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERLEUKINS.
SUBBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL-7 A:
PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: DEFECTS IN ILZRG ARE THE CAUSE OF A CANINE X-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: COMMON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEVERE COMBINED IMMUNODEFICIENCY
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunodeficiency
                               HEMATOPO_REC_S_F1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT FOR THE RECEPTORS FOR A VARIETY OF
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Glycoprotein;
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Pred. No. 9.9e-102;
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; Fissipedia; Canidae;
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  Signal
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CARBOHYD
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01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Cytokine receptor common gamma chain precursor (Ginterleukin-2 receptor gamma chain) (IL-2R gamma
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                                                                                                                                                                                              gamma gene.";
DNA Cell Biol. 15:453-459(1996).
-!- FUNCTION: COMMON SUBUNIT FOR
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE-96268473; PubMed-8672241;
Yoo J., Stone R.T., Solinas-Toldo
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                 between
                                                                                                                                                                                                                                                   "Cloning
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                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
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               ween the Swiss Institute of Bioinformatics Institute.
                                                                                    SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN
                                                                                                                                                     INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO
                                                                                                                                             PROBABLY ALSO THE IL-13
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                                                    SWISS-PROT entry is copyright. It is produced through a
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                                                                                                                                                                                                                                                                                                                                                                                                              (Bovine)
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82.8%;
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                                                                                                                                             RECEPTORS
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CYTOKINE RECEPTOR COMMON GAMMA
EXTRACELLULAR (POTENTIAL).
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No. 1
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ovine interleukin-2
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mma chain)
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InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III
InterPro; IPR003531; Hematc
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TRANSMEM
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Cytokine receptor common gamma chain precursor (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL-2R gamma chain)
Biochem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _MOUSE
CYRG_MOUSE
                                                        MEDLINE=93277575; PubMed=8503926; Kumaki S., Kondo M., Takeshita T., A "Cloning of the mouse interleukin 2 demonstration of functional differen receptors.";
                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
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Similarity 76.2%;
82; Conservative 2
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                        Biophys.
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Metazoa; Chordata; C
Metazoa; Rodentia; S
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

FIBRONECTIN TYPE-III.

POTENTIAL.

POTENTIAL.

POTENTIAL.

POTENTIAL.

N-LINKED (GLCNAC. ..) (POTEN-LINKED (GLCNAC. .
                                                                             differences
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Pred. No. 1.4e-76;
1; Mismatches 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOKINE RECEPTOR COMMON GAMMA CHAIN
                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                          193:356-363(1993)
                                                                                                                        Asao
                                                                                                receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 369
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                                                                                                Nakamura M.,
r gamma chain
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(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                           mouse
                                                                                                                                                                                                                                                       Murinae; Mus
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                                                                                                                           Sugamura K.;
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     EMBL; D13821; BAA02974.1; -.

EMBL; D13565; BAA64279.1; -.

EMBL; D13565; BAA02760.1; -.

EMBL; L20048; AAA39286.1; -.

EMBL; S75842; AAB32904.1; JOINED.

EMBL; S75844; AAB32904.1; JOINED.

EMBL; S75847; AAB32904.1; JOINED.

EMBL; S75848; AAB32904.1; JOINED.

EMBL; S75848; AAB32904.1; JOINED.

EMBL; S75849; AAB32904.1; JOINED.

EMBL; S75850; AAB32904.1; JOINED.

EMBL; S75851; AAB32904.1; JOINED.

EMBL; X75337; CAAS3085.1; -.

PIR; JN0592; JN0592.

PIR; JN0592; JN0592.

PIR; JN0775; JN0775;

INTERPRO; IPR00351; Hematopo_receptor_S_F1.

InterPro; IPR003961; FM_III.

InterPro; IPR003961; FM_III.
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SEQUENCE FROM N.A.
MEDLINE-93366191; PubMed-8359699;
Kobayashi N., Nakagawa S., Minami Y.
Kobayashi P. A Fequencing of the CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bloinformatics Institute. There are no restricted the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion 
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"Molecular mechanisms
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Disanto J.P., Certain S., Wilson A.,
Fischer A., de Saint Basile G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a or send an email to
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STRAIN-CBA/CA;
                                                                                                   Pfam; PF00041; fn3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ne adhesion protein CD44.";
Neurooncol. 26:231-239(1995)
- FUNCTION: COMMON SUBUNIT FO
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SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL
PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130:303-304(1993).
                                                   PS01355; HEMATOPO_REC_S_F1; 1.
  Transmembrane; Glycoprotein; Signature 1 22 BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-2 receptor gamma
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RESULT 5

1132_HUMAN STANDARD; PRT; 380 AA.

ID 1132_HUMAN STANDARD; PRT; 380 AA.

AC Q14627; 000667;

DT 01.NOV-1997 (Rel. 35, Created)

DT 01.NOV-1997 (Rel. 35, Last sequence update)

DT 30.MAY-2000 (Rel. 39, Last annotation update)

DE Interleukin-13 receptor alpha-2 chain precursor (Index of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the contr
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Best Local Similarity
Matches 156; Conser
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                                                                                                                                                                                                                                                       chain.
  TISSUE-Brain;
MEDLINE=97321053; PubMed-9177784;
Guo J., Aplou F., Mellerin M.P., 1
"Chromosome mapping and expression
                                                                                                                                                                                                                                                                                                                                 TISSUE-Renal cell
MEDLINE=96279273;
Caput D., Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                               Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H., Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                      "Cloning and characterization of a specific intending protein structurally related to the IL-5
                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                            TISSUE=Testis;
                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                  Ferrara P.;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                               nal cell carcinoma;
5279273; PubMed=8663118;
Laurent P., Kaghad M.,
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POTENTIAL.
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Pred. No. 4.
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  Lebeau B.
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i.9e-65;
les 42;
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TYPE-III.
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  interleukin-13
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Matches 60
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01-NOV-1997
01-NOV-1997
16-OCT-2001
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SEQUENCE
                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-13 receptor alpha-1 chain precursor
13RA-1) (Interleukin-13 binding protein) (NR4).
IL13RA OR IL13RA OR IL13R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; x95302; CAA64617.1; -.
EMBL; U70981; AAB17170.1; -.
EMBL; Y08768; CAA70021.1; -.
MIM; 300130; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (IL-13), BUT NOT TO IL-4.
-:- SUBCELULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: COUPAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       receptor.";
Genomics 42:141-145(1997).
-!- FUNCTION: BINDS AS A MONOMER
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InterPro; IPR003532;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP-----T
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPRE--PRRQ 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGSE-VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSW-----KPGIGVLLDT
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TE; PS01356; HEMATOPO_REC_S_F2; 1.
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    Metazoa;
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Chordata;
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FN_III.
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POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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  Craniata;
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No. 2e-10;
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    Vertebrata;
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    Euteleostomi;
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CCCCCCCRRRRRRRNCOC

Willson T.A.; MEDLINE-96133964; NCBI_TaxID=10090;

Hilton D.J., Zhang J.-G., SEQUENCE FROM N.A.

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                                                                                                                                                                                                                                                                   ELKCIWHNLSYMKCSWLPGRNTSPDTHYTLYYMY--SSLEKSRQCENIYREGQHIACSFK 186
                                                                                                                                                                                                                                                                                                                     EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSH-YLFSEEITSGCQ
                                                        NPQNFRSRCLTYEVEVNNTQTDRHNILEVEEDKCQNSESDRNMEGTSCFQLPGVLADAVY
                                                                                                          N--RFLNHCLEHLVQY---RTD-----WDHSWTEQSVDYRHKFSLPSVDGQKRY
                                                                                                                                                               LTKVEPSFEHQNVQIMVKDNAGKIRPSCKIVSLTSYVKP-DPPHIKHLLLKNGALLVQWK
                                                                                                                                                                                                              LQKKEIHL-YQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWN
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Pred. No. 3.2e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 424;
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(POTENTIAL).
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I131_HUMAN
P78552; Q996
                                                                                     or send an
                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bloinformatics and the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was modified and this statement is not removed. Usage by and for commercia entitles requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wada M., Hisano T., Kuwano M.;
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-
ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN
ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA
CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF
GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.
-i- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPANY
-i- SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPANY
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EMBL; Y10659; CAA71669.1;
EMBL; Y09328; CAA70508.1;
EMBL; U62858; AAB37127.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "cDNA cloning and characterization of receptor alpha chain.";
J. Biol. Chem. 271:29265-29270(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last sequence update)
30.MAY-2000 (Rel. 39, Last annotation update)
Interleukin-13 receptor alpha-1 chain precursor (IL-13R-alpha-1) (IL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aman M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97067184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Miloux B., Laurent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rissue=B-cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning of the human IL-13R alpha1 chain and reconstitution with the IL4R alpha of a functional IL-4/IL-13 receptor complex.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  errara P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WEDLINE=97165986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 TVRVRVKTNKLCFDDNKLWSDWS
                                                                                                                                                                                                                                                                                                            IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS.
SUBCELLULAR LOCATION: Type I membrane protein.
TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER,
SKELETAL MUSCLE AND OVARY; LOWEST LEVELS IN BRAIN, LUNG AND
KIDNEY, ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
KIDNEY, ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.
SIMILARITY: CONTAINS 1 IMMUNOSLOBULIN-LIKE C2-TYPE DOMAIN.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q99656;
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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t P., Bonnin O.,
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N., Obiri N.I.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Puri R.K., Modi W.S.,
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                                                                                                                                 http://www.isb-sib.ch/announce/
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ells T.,
                                                                                                                                                                                                                                              collaboration
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MGD; MGI:105052; Ill3ral.

InterPro; IPRO02996; CR1A. InterPro; IPRO03532; Hemat PROSITE; PS01356; HEMATOPC

Transmembrane;

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SIMILARITY)

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246 154 187

198

TFRVRSRFNPLC-GSAQHWSEWS

Query Match Best Local S Matches 56

Similarity

14.18; 27.68;

Conservative

129 95

37

CARBOHYD CARBOHYD SEQUENCE

48402

MW;

DISULFID DISULFID DISULFID CARBOHYD

26 26 341 365 37 44 132 171 35 59 103 103 136 262 338

CARBOHYD

DOMAIN TRANSMEM

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Best Local
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SIGNAL 1 21
CHAIN 2 427
DOMAIN 344 367
DOMAIN 368 427
DOMAIN 369 427
DOMAIN 39 102
DISULFID 134 144
DISULFID 173 185
CARBOHYD 37 37
CARBOHYD 37 37
CARBOHYD 105 105
CARBOHYD 105 105
CARBOHYD 157 157
CARBOHYD 157 157
CARBOHYD 255 265
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CARBOHYD 265 265
CARBOHYD 293 293
CARBOHYD 329 329
CARBOHYD 341 341
CONFLICT 130 130
CONFLICT 130 130
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P32927;
01-OCT-1993 (Rel.
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CONFLICT
CONFLICT
SEQUENCE
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                                                                                                              Cytokine receptor common CSF2RB OR IL5RB OR IL3RB.
                                                                                                                                    01-FEB-1996 (Rel. 16-OCT-2001 (Rel.
            Miyajima
                                 SEQUENCE FROM N.A.
MEDLINE=91088571; PubMed=1702217;
                                                                            Mammalia; Eutheria; Primates;
                                                                                        Eukaryota; Metazoa;
                                                                                                  Homo sapiens (Human)
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Pfam; PF00041; fn3; 1.
                      Hayashida K., Kitamura
                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR003961;
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                                                                                                                                                                                                                                                                                                                                          QLQKKEIHLYQTFVVQL--QDPREPRRQATQMLKLQNLVIPWAP--ENLTLHKLSESQLE 149
                                                                                                                                                                                                                                       GVLPDTLNTVRIRVKTNKLCYEDDKLWSNWSQEMSIG
                                                                                                                                                                                                                                                                                                                                                                                             EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGC--
                                                                                                                                                                                                                                                          SVDGQKRYTFRVRSRFNPLC-GSAQHWSEWSHPIHWG
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58; Conser
            Α.;
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 cloning of
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                                                                                                                                                                                STANDARD;
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                                                                                                                              27, Created)
33, Last sequence update)
40, Last annotation update)
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                                                                                        Chordata;
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26.7%;
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 a second subunit of
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POTENTIAL.
                       Gorman D.M., Arai K.,
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N-LINKED
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POTENTIAL.
BY SIMILARITY.
BY SIMILARITY.
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                                                                            Catarrhini;
                                                                                        Craniata; Vertebrata;
                                                                                                                         chain
                                                                                                                                                                               PRT;
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No. 6.4e-08
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I (IN REF. 3).
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the receptor for human
                                                                            Hominidae; Homo
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                                                                                                                       (CDw131 antigen).
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                        Yokota T.,
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(POTENTIAL).
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                                                                                        Euteleostomi;
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PIR; A39255; A39255.
HSSP; P19235; 1EBA.
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-i- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, INT-
-ND GRANULCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.
-i- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE
CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; P19235
MIM; 138981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS01355; HEMATOPO_REC_S_F1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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Biochem. Biophys. Res. Commun. 18
-!- FUNCTION: THIS IS A RECEPTOR
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an email to license@isb-sib.ch).
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IPR003961; FN_III.
IPR003528; Hematopo_receptor_L_F1
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Granulocyte-macrophage colony-stimulating factor receptor alpha chain precursor (GM-CSF-R-alpha) (GMR) (CDW16) (CD116 antigen).
(CSF2RAX OR CSF2RA OR CSF2R OR CSF2RX) AND
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granulocyte-macrophage colony stimulating factor receptor.
                                      MEDIINE-91376112; PubMed-1832774;
Raines M.A., Liu L., Quan S.G., Joe V., DiPersio "Identification and molecular cloning of a solub. macrophage colony-stimulating factor receptor.";
Proc. Natl. Acad. Sci. U.S.A. 88:8203-8207(1991)
                                                                                                                                                                              TISSUE=Placenta;
MEDLINE=91088339; PubMed=2148207;
                                                                                                                                                                                                                                        Crosier K.E., Wong G.G., Mathey-Prevot B., Nathan D.G., Sieff C.A.; "A functional isoform of the human granulocyte/macrophage colony-stimulating factor receptor has an unusual cytoplasmic domain."; proc. Natl. Acad. Sci. U.S.A. 88:7744-7748(1991).
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MEDLINE=91352066; PubMed=1715577;
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J. Biol. Chem.
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"Cloning of a potentia
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Hu X., Emanuel P.D., Zuckerman K.S.;
PCloning and sequencing of the CDNAs encoding two alternative
splicing-derived variants of the alpha subunit of the granulocyte-
macrophage colony-stimulating factor receptor.";
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ALTERNATIVE PRODUCTS: 6 ISOFORMS; 1 (SHOWN HERE), 2, 3, 6; ARE PRODUCED BY ALTERNATIVE SPLICING.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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PS01356; HEMATOPO_REC_S_F2; 1.
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 (GLCNAC
                                                                                                                                         Signal;
                                                                                                                                         Alternative splicing
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SEQUENCE O TISSUE=Ova Pitts G.R.	gallopavo. Biol. Repr [2]	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE=Kidney; MEDLINE=97057891; Pub Zhou J.F., Zadworny D "Molecular cloning, t prolactin receptor du	Meleagris gallopa Eukaryota; Metazo Archosauria; Aves NCBI_TaxID=9103;	01-NOV-1997 (R 01-NOV-1997 (R 15-JUL-1999 (R Prolactin rece	SULT 11 CLR_MELGA PRLR_MELGA CQ91094; Q9	312 AIEFG	221 PIHWGSN	161 LEHLVQ : : 266 TENLL-	07 D	108 VQLQDP	9	64 TLHYW	5 ILTPN-0 : 109 LLYPNSO	Query Match Best Local Si Matches 52;	SEQUENCE	VARSPLIC VARSPLIC	VARSPLIC		VARSPLIC VARSPLIC	VARSPLIC VARSPLIC	CARBOHYD CARBOHYD CARBOHYD VARSPLIC
)F 82-121 (ry; , You s.:	"; od. 55:1	ROM N.A. ney; 057891; Zadworn cloning receptor	gallopavo Metazoa; .a; Aves; .=9103;	0000	· · · ·	SD 318	SN 227	QxxTUWUH	TKKIERFN	RE	: : IRNSKRRR	TLHYWYKNSDNDKVOKC	GNEDTTADFF	imilarity; Conser	400 AA;	334 376	318		287 316	234 271	229 272 305 216
AND 473-	1	Meo is:	o (Common tur ; Chordata; (Neognathae;	1. 35, Created 1. 35, Last se 1. 38, Last an tor precursor	TANDARD; Q91092;			SWIEQSVD	PPSNVTVR	PRRQATQMI	: : : EIRCPYYI	VOKCSHYLF	GNEDTTADFFLTTMPTDS	11.4%; 21.1%; vative	46206 1	400 400	333		400 400	400 286	229 272 305 233
·522 FROM N.A. •x D.N., el Halawani M.E.;		i=8902221; Guemene D.,'Kuhnlein U.; sue distribution, and expression of the ng various reproductive states in Meleagris	ı turkey). .a; Craniata; Vertėbrata; Euteleostomi; nae; Galliformes; Meleagrididae; Meleagris.	ted) sequence update) annotation update) or (PRL-R) (TPRLR).	PRT; 831 AA.			EHLYQYKIDWDHSWIEQSVDYKHKESLESVDGQKKYIFKVRSKENELCGSAQHWSEWSH 220 : : 	VHRKNTQPG 26	PRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHC 160	DSGTHVGCHLDNLSGLTSRNYFLVNGTSREIGIQFF 20	SEEITSGCOLOKKEI	IDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNL 63 :: : : :: A 1 ::	Score 146.5; DB 1; Length 400; Pred. No. 2.7e-05; 44; Mismatches 90; Indels 61; Gaps 10;	4;	MISSING (IN ISOFORM 3). MISSING (IN ISOFORM 3). ITWEETTPEEGKGYREBVLTVKBIT -> MGPORHHRGGWN ITWEETTPEEGKGYREBVLTVKBIT -> MGPORHRGGWN ITWEETTPEEGKGYN	DDGNLGSVYIYVLLIV -> LGYSGCSRQFHRSKTN (IN	PPVQIKOKLNUMHEVEDEILWEFTTPEEGKGTREEVITVK EIT -> DDHLGGIHPRGRERLPRRGLDREGNYLRPRGCRN GMDISASATRGNCFLDDAVNLYIIFYVFI (IN ISOFORM	MISSING (IN ISOFORM 4). MISSING (IN ISOFORM 4). GSDDGNLGSVYIYVLLIVGTLVCGIVLGFLFKRFLRIQRLF	MISSING (IN ISOFORM 6). HISSING (IN ISOFORM 6). INVSGDLENRYNEPSS -> VVLTTGTSALCTEMCS (IN	N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-LINKED (GLCNAC) (POTENTIAL). ERRNPPSNYTYRCNTTHC -> GSLGYSGCSRQFHRSKTN

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SIGNAL
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 3.
PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
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EMBL; U22947; AAA75038.1; -.
EMBL; U22924; AAA75039.1; -.
HSSP; P16471; 1BP3.
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SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                       YRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWS
                                                                                                                                                                                            ECPDYR-----TSGPNSCYFNRNYTNSWTTYNITVTATNEIGSNSSDPQYVDVTSIVQPG
                                                                           VQTQCKINRLNAGMRYVVQVRCMLDP----GEWSEWS
                                                                                                                                                                APENLTLHKLSESQLELN-----WNNRFL----NHCLEHLVQYRTDWDHSWTEQSVD
                                                                                                                                                                                                                       KCSHYLFSEEITSG----CQLQKKEIHLYQTFVVQLQDPREPRRQAT--QMLKLQNLVIPW
                                                                                                                                                                                                                                                     LTTVGLTSQSFPGKP-KIIRCRSLEKETFSCWWKPGSDGGLPTNYTL--FYSKDSEEKIY 73
                                                                                                                                                                                                                                                                               LTIMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQ 78
                                                                                                                                                                                                                                                                                                             53; Conservative
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ION: THIS IS A
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    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Glycoprotein;
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FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
FIBRONECTIN TYPE-III 3.
FIBRONECTIN TYPE-III 4.
BY SIMILARITY.
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CYTOPLASMIC
FIBRONECTIN
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Pred. No. 8e-05;
6; Mismatches
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KKEIHLYQTFVVQLQDPREPRRQAT - - QMLKLQNLVIPWAPENLTLH - - - KLSESQLELN IRCRSLEKETFSCWWKPGSDGGLPTNYTL - - FYSKDSEEKIYECPDYGMSG - - PNSCYFD VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQ

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CHAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Cropsac;
MEDLINE=94283267;
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15-JUL-1998
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01-NOV-1997
                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                     PROSITE; PS01352;
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hematopo_receptor_L_F1.
Pfam; PF00041; fn3; 4.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Endocrinology 135:269-276(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chen X., Horseman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prolactin
                                                                                                                                                                                                                                              Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor."
                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROLACTIN
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         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor
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Conservative
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N.D.;
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35, Last sequence update)
36, Last annotation update)
                                                                                                                                                                                                                                                     HEMATOPO_REC_L_F1;
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        10.3%;
22.2%;
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                                               MW;
37;
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Pred. No. 0.007; Mismatches
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BY SIMILARITY.
N-LINKED (GLCN)
         Score 132.5;
Pred. No. 0.
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RESULT 13
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01-AUG-1990
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                  "The murine interleukin-4 receptor: molecular cloning and characterization of secreted and membrane bound forms."; Cell 59:335-348(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mosley B., Beckmann M.P., March C.J., Idzerda R.L., Vandenbos T., Friend D., Alpert A., Anderson D., Jac Wignall J.M., Smith C., Gallis B., Sims J.E., Urdal Cosman D., Park L.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IL4R_MOUSE P16382;
                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                        use by non-profit institutions as long as modified and this statement is not removed. \ensuremath{\mathbb{C}}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                        InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN_III.
InterPro; IPR003531; Hematopo_receptor_S_F1.
                                                                                                                                                                                                                                      the European Bioinformatics Institute.
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               Pfam; PF00041; fn3; PROSITE; PS01355; H
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                                                                                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through a collaboratic een the Swiss Institute of Bloinformatics and the EMBL outstation surgean Bioinformatics Institute. There are no restrictions on it by non-profit institutions as long as its content is in no war by non-profit institutions.
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(Rel. 35, Last annotation update)
-4 receptor alpha chain precursor
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Glycoprotein; Signal; Alternative splicing
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Eukaryota; Metazoa; (
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                                                                                                                                                                                   OC. Natí. Acad. Sci. U.S.A. 87:5459-5463(1990).

FUNCTION: HIGH AFFINITY RECEPTOR FOR INVERLEKIN-3, INTE AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR.

SUBGNIT: HETERODIMER OF AN ALCHA AND A BETA CHAIN. THE B CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.

CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.

SUBCELLULAR LOCATION: Type I membrane protein.

SUBCELLULAR LOCATION: Type INFORMATION TYPE III-LIKE DOMAINS.

SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation.
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221 OR AIC2B OR IL3RB1.
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C MEDILINE-93246019; PubMed-1338725;
X MEDILINE-93246019; PubMed-1338725;
X MEDILINE-93246019; PubMed-1338725;
X MEDILINE-93246019; PubMed-1338725;
X MEDILINE-93246019; PubMed-1338725;
X MEDILINE-93246019; PubMed-1338725;
X MEDILINE-93246019; PubMed-1338725;
X Molecular cloning of the bovine prolactin receptor and distribution of the prolactin and growth hormone receptor transcripts in fet utero-placental tissues.";
X MOLICELL Endocrinol. 89:47-58(1992).

RL MOL Cell. Endocrinol. 89:47-58(1992).
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Best Local S
Matches 48
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15-JUL-1998
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Mammalia; Eutheria;
Bovidae; Bovinae; Bo
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or send a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro, IPR002996; CRIA.
InterPro, IPR002982; Cytok_receptor_2.
InterPro, IPR003961; FN_III.
InterPro, IPR003531; Hematopo_receptor_S_F1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
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A35782; A35782.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ESQLELNWNNR-----FLNHCLEHLVQYR----TDWDHSWTEQSVDYRHKFSLPSVDGQKR
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48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                  receptor precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                          (Bovine).
                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 35, Created)
(Rel. 35, Last sequence update)
(Rel. 36, Last annotation update)
eceptor precursor (PRL-R).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23
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99111 MW;
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4463
896
241
440
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62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.7%;
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BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

N-LINKED (GLCNAC. . .) (POTENTIAL)

BCE16EDFDC07A999 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.005; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PÓTENTIAL.

CYTOKINE RECEPTOR COMMON BETA EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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. 0.0047;
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                                                                                                                                                                                                                                                                                                                           Pecora; Bovoidea;
                                                   PITUITARY HORMONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                     distribution fetal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42;
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Best Local Similarity
Matches 60; Conserv
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DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR00328; Hematopo_receptor_L_F1
Pfam; PF00041; fn3; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L02549; AAA51417.1; -. HSSP; P14787; 1AN3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00060; FN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a
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 173
                       169
                                                130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS.4 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROLACTIN.
KPEKATDWETHFTLKQTQLK-IFNL--YPGQK---YLVQIRCKPDHG--
                                                                                                                      CSHYLFSEEITSG----CQLQKKEIHLYQTFVVQL----
                                                                                                                                                                         LSVSTL---PLPE----VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQK 79
                                                              QATQMLKLQN------LVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYR----
                                                PANLTLELKHPEDRKPYLWIKWSPPTMT-----DVKSGW---
                                                                                                CPDYK----TGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLYVHVTYIVEPEP
                                                                                                                                                 LSVSLLNGQSPPEKPKLVKCRSPGKETFTCWWEPGADGGLPTNYTLTY-HKEGET-LIHE
                                                                                                                                                                                                                                                                                                                                                                                                                            PS01352;
                       -TDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane;
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                         24
581
234
258
258
1122
122
227
227
46
86
86
5153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                              9.4%;
                                                                                                                                                                                                                                                                                                                                                                                                  Glycoprotein;
POTENTIAL.
                                                                                                                                                                                                                                                                W.
                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).

POTENTIAL.

POTENTIAL).

PIBRONECTIN TYPE-III 1.

FIBRONECTIN TYPE-III 2.

BY SIMILARITY.

N-LINKED (GLUNAC. . .) (POTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).

N-LINKED (GLUNAC. . .) (POTENTIAL).
                                                                                                                                                                                               Score 121.5; DB 1;
Pred. No. 0.0055;
0; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                        PROLACTIN RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         There are no rest
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interlenxin z rece	titin, cardiac mus	prolactin receptor	prolactin receptor	prolactin receptor	prolactin receptor	proto-oncogene - m	hematopoietic grow	interleukin-4 rece	somatotropin recep	interleukin-6 sign	glycoprotein 130 -	granulocyte-macrop	interleukin-2 rece	interleukin-5 rece	prolactin receptor	

ALIGNMENTS

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Accession: A55718
Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, idenomics 23, 69-74, 1994
A;Title: IL-2Rgamma gene microdeletion demonstrates the A;Reference number: A55718; MUID:95130114
A;Accession: A55718
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-373 <HEN>
A;Cross-references: GB:U04361; NID:9517411; PIDN:AAC48.
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication
                                                                                   R;Cao, X.; Kozak, C.A.; Liu, Y.
Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468,
A;Title: Characterization of cDNAs encoding t
A;Reference number: A47514; MUID:93391374
A;Accession: I49280
A;Status: preliminary; translated from GB/EMB
A;Residues: 1-369 <CAO>
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A;Cross-references: EMBL:U21795; NID:g727349; A;Accession: A47514
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-369 <RE2>
                                                                                                                                                                                                       C;Species: Mus musculus (house mouse)
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change C;Accession: I49280; A47514; JN0592; JN0775; S37582; I53398 R;Cao, X.; Kozak, C.A.; Linch and B464-8469 1993
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C;Species: Canis lupus familiaris (dog)
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-
                                                                                                                                                                                                                                                                                 interleukin-2 receptor gamma chain precursor - mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNSTVPMPNGNEDITPDFFLTATPSETLSVSSLPLPEVQCFVFNVEYMNCTWNSSSEPRP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNLTLHYWYKNSNDDKVQECGHYLFSREVTAGCWLQKEEIHLYETFVVQLRDPREPRRQS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Felsburg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85.2%;
82.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1097; DB 2;
Pred. No. 7.1e-84;
                                                                                                                              from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-Aug-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:AAC48403.1; chain
                                                                                                                                                                                the murine
                                                                          PIDN:AAA64279.1; PID:g727350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #text_change 23-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that canine X-linked severe combined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 373;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                interleukin
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                                                                                                                                                                                                                                                                                                                                                                              254
                                                                                                                                                                                                                                                     20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                                                2 receptor (IL-2R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                         QΥ
                                                                                                                                                                              Дb
                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                   В
                                                                                                                                                                                                                                                                                   QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: IL-2Rgamma
A;Introns: 39/1; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-369 < KOB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: JN0775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-369 < KU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: JN0592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                          181
                                                                                                           144
                                       204
                                                                                                                                             122
                                                                                                                                                                                84
                                                                                                                                                                                                                    62
                                                                                                                                                                                                                                                   24
                                                                                                                                                                                                                                                                                        N
                                       HEPRESLPSVDELKRYTERVRSRYNPICGSSQQWSKWSQPVHWGSHTVEEN
                                                                          DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN
                                                                                                                                                                                                                                                                                                                            156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-369 <KUM>
                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA
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A;Description: receptor for interleukin-2
A;Pathway: interleukin-2 stimulated growth and differentiation of T cell
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; glycoprotein; transmembrane
F;1-22/Domain: signal sequence #status predicted <STG>
F;23-369/Product: interleukin-2 receptor gamma chain #status predicted <
F;256-284/Domain: transmembrane #status predicted <TMM>
F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene 130, 303-304, 1993
A:Title: Cloning and sequencing
A:Reference number: JN0775; MUII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:L20048; NID:g404067; PIDN:AAA39286.1; PID:g404068 R;Kumaki, S.; Kondo, M.; Takeshita, T.; Asao, H.; Nakamura, M.; Sugamura, K. Biochem. Biophys. Res. Commun. 193, 356-363, 1993 A;Title: Cloning of the mouse interleukin 2 receptor gamma chain: Demonstration A;Reference number: JN0592; MUID:93277575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, P.; Fischer, A.; de Eur. J. Immunol. 24, 3014-3018, 1994
A:Title: The murine interleukin-2 receptor gamma chain gene: organization, chromosoma A; Reference number: I53398; MUID:95104285
A; Accession: I53398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; PID:g303685
R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono, T.
Gene 130, 303-304, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-350,'S', 352-366,'S', 368-369
A; Cross-references: EMBL: X75337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S37582
A; Accession: S37582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Chiu, R.K.; Dougherty, G.J. submitted to the EMBL Data Library, October 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Introns: 39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3 C; Complex: The high affinity receptor is a heterotrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNAA;Residues: 1-369 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Description: Regulation of CD44-mediated cellular adhesion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: nucleic acid sequence not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:D13821; NID:g436045;
                                               QMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFL-NHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                     NLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQAT 121
                                                                                                                                                                                                                                                            NTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVENVEYMNCTWNSSSEPQPT 61
NLTLHYRYKVSDNNTFQECSHYLFSKEITSGCQIQKEDIQLYQTFVVQLQDPQKPQRRAV 143
                                                                                                                                                                                                                              SSKVLMSSANEDIKADLILTSTAPEHLSAPTLPLPEVQCFVFNIEYMNCTWNSSSEPQAT
                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                    66.3%;
67.2%;
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MUID:93366191
                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                 853.5; DB 2
No. 1.3e-63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286/2; 308/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                encoding a mouse IL-2 receptor gamma.
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                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cells, B
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A;Mclecule type: mRNA
A;Residues: 1-897 <ARAY
A;Residues: 1-897 <ARAY
A;Cross-references: GB:M38275
C;Comment: The human high-affinity IL-3, IL-5, and GM-CSF receptors have ligand-s
C;Genetics:
A;Gene: GDB:CSF2RB
A;Cross-references: GDB:126838; OMIM:138981
A;Cross-references: GDB:126838; OMIM:138981
C;Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C;Keywords: alternative splicing; cytokine receptor; duplication; transmembrane F;17-16/Domain: signal sequence #status predicted <SIG>F;17-897/Product: cytokine receptor common beta chain #status predicted <MAT>
F;35-232/Domain: extracellular #status predicted <EXT>
F;35-232/Domain: cytokine receptor homology <CRS2>
F;444-460/Domain: transmembrane #status predicted <ININ>
F;461-897/Domain: intracellular #status predicted <ININ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Res. Commun. 287, 969-976, 2001
A;Title: Expression of a functional II-13Ralphal by A;Reference number: JC7773, PMID:11573960
A;Rocession: JC7773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: A39255
C;Accession: A39255
R;Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
Proc. Natl. Acad. Sci. U.S.A. 87 account subunit of the receptor Title: Molecular cloning of a second subunit of the receptor Paference number: A39255; MUID:91088571
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A; Residues: 1-426 <PIE>
A; Cross-references: GB:AY044251
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C;Accession: JC7773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cytokine receptor common beta chain precursor - C;Species: Homo sapiens (man) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-19 C;Accession: A39255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
A39255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IL-13Ralpha
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Best Local S
Matches 54
Best Loc
Matches
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                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLTKVESNYEHHNIQIMVKDNAGKIRPSYKIVSFTSNVKPGPPHIKHLF-LKNGALFVQW 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQL 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TVYTVRVRVKTNKLCFDDNDLWSNWSEALSIG 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NN - - RFLNHCLEHLVQYRTDWDHSWTEQSVDYRHK - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELQCTWHNLSYMKCSWLPGKNTSPDTNYTLYYWY -- SSLGKSLQCEN-IHREGQHIGCSF 185
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54; Conser
l Similarity
55; Conser
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Conservative
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                  12.3%;
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40;
                  Score
Pred.
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Pred. No. 1.7e-06;
0; Mismatches 101;
Mismatches
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                  159;
"7 2.
DB 1; 1
2.6e-05;
nes 79;
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                                      Length 897;
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  34;
                                                                                                                                                                                                                                                           transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human granulocyte-ma
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Gaps
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R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA A;Reference number: JQ1655; MUID:93075121
A;Accession: JQ1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prolactin receptor precursor - chicken G;Species: Gallus gallus (Chicken) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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F;1-23/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Superfamily: cytokine receptor homology C; Keywords: glycoprotein; transmembrane p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Experimental source: kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Residues:
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A; Residues: 1-831 <TAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession: JQ1655
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Matches
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nes 50; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRFLNHCLEHL-----VQYRTD----WDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QIPVPDPATHGQYIVSVQ----PRR-AEKHIK-SSVNIQMAPPSLNVTKDGDS-YSLRWE 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWN 153
  TLDP-----GEWSEWSSERH
                                    RFNPLCGSAQHWSEWSHPIH
                                                                           WAKWSPPLLADASSNHLYHYELRIKPEEKEEWETISVGVQTQCKINRLNAGMRYVVQVRC
                                                                                                                                                                                                                                  IRCRSLEKETFSCWWKPGSDGGLPTNYTL--FYSKDSEEEIYECPDYR----TSGPNSC
                                                                                                                                                                                                                                                               VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSG---C
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                                                                                                                -- NWNNRFL-----NHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRS
                                                                                                                                                     YFNKNHTSPWTTFNITVTATNEIGSNSSDPQYVDVTSIVQPGSPVNLTLETKRSANIMYL
                                                                                                                                                                                        QLQKKEIHLYQTFVVQLQDPREPRRQAT--QMLKLQNLVIPWAPENLTLH-KLSESQLEL
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25.0%;
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Pred. No. 0.00013;
4; Mismatches 90
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C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change C;Accession: S06945; A41286; A44474
R;Gearing, D.P.; King, J.A.; Gough, N.M.; Nicola, N.A. EMBO J. 8, 3667-3676, 1989

granulocyte-macrophage colony-stimulating factor receptor A N,Alternate names: GM-CSF receptor alpha chain; hemopoletic

precursor - hu growth factor

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Molecule type: DNA

(Residues: 'M',377-400 < RAP>
A; Cross-references: GB:S48539; NID:g258858; PIDN:AAB23942.1;
A; Note: sequence extracted from NCBI backbone (NCBIP:117980)
C; Genetics:
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A;Gene: GDB:CSF2RA; CSF2R
A;Cross-references: GDB:11877; OMIM:306250; OMIM:425000
A;Cross-references: GDB:11877; OMIM:306250; OMIM:425000
A;Map postition: Xp23.32-Xp22.32; Yp11.3-Yp11.3
C;Keywords: glycoprotein; growth factor receptor; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>F;1-22/Domain: granulocyte-macrophage colony-stimulating factor receptor #status predicted <TMM>F;322-446/Domain: transmembrane #status predicted <TMM>F;46,54,99,123,135,182,195,223,229,272,305/Binding site: carbohydrate (Asn) (covalent)
                                          R;Ashworth, A.; Kraft, A.
Nucleic Acids Res. 18, 7178, 1990
A;Title: Cloning of a potentially soluble receptor A;Reference number: S13684; MUID:91088339
A;Accession: S13684
                                                                                                                                                 granulocyte-macrophage colony-stimulating factor receptor - human C;Species: Homo sapiens (man) C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 05-Nov-1999 C;Accession: S13684; A40989
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S13684
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Genomics 14, 455-461, 1992
A;Title: Arrangement and localization of the human GM-CSF receptor alpha chain A;Reference number: A44474; MUID:93052350
A;Accession: A44474
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A; Molecule type: mRNA
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                       A; Status: preliminary; translation not shown
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                        312 AIEFGSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 LEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 146.5; DB 2;
Pred. No. 0.00011;
4; Mismatches 90;
                                                                                           for
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
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    152
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                                                                                                                                     251
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  WNNR-----FLNHCLEHLVQYRTD---WDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRS
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C;Superfamily: interleukin-3 receptor beta chain; c;C;Keywords: cytokine receptor homology <CRS1>F;39-235/Domain: cytokine receptor homology <CRS2>F;253-433/Domain: cytokine receptor homology <CRS2>
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A; Residues: 314-333 <RAI>
A; Cross-references: GB: M73832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-333 <ASH>
A;Cross-references: EMBL:X54935; NID:g31860; PIDN:CAA38697.1; PID:g31861
A;Cross-references: EMBL:X54935; NID:g31860; PIDN:CAA38697.1; PID:g31861
R;Ratnes, M.A.; Liu, L.; Quan, S.G.; Joe, V.; DiPersio, J.F.; Golde, D.W.
Proc. Natl. Acad. Sci. U.S.A. 88, 8203-8207, 1991
A;Title: Identification and molecular cloning of a soluble human granulocyte-macropha A;Reference number: A40989; MUID:91376112
A;Accession: A40989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-896 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Neurosci. 15, 5800-5809, 1995
A;Title: Cloning of rat interleukin-3 receptor beta-subunit
A;Reference number: I56563; MUID:95370942
A;Accession: I56563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Appel, K.; Buttini, M.; Sauter, A.; Gebicke-Haerter, P.J. J. Neurosci. 15, 5800-5809, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Rattus.sp. (rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    interleukin-3 receptor beta-subunit -
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                                                                                                                                                                  38 VQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64 TLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQ-------KKEIHLYQTFV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 ILTPN-GNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQPTNL 63
HCSLNVSDPAAHSQYTVSVK-----RLEQGKFIESFN-HIQMNPPTLNLTKNRDS-YSLH
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                                                    -CQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELN 151
                                                                                                           LQCFFDGIQSLNCSWEVWTK-VTDSVSFGLFYSSSPKAGEKKCSPVV--KELQASRYTRY 307
                                                                                                                                                                                                                      1 Similarity
48; Conserv
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52; Conserv
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                                                                                                                                                                                                                         Conservative
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21.1%;
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                                                                                                                                                                                                                                                      Pred.
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                                                                                                                                                                                                                                                      Score 136.5; DB Pred. No. 0.0019
                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                         29;
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                                                                                                                                               prolactin receptor - pigeon
c;Species: Columba livia (domestic pigeon)
C;Date: 13-Sep-196 #sequence_revision 13-
C;Accession: I50455
R;Chen, X; Horseman, N.D.
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submitted to the EMBL Data Library, March 1994
A:Description: Cloning and sequencing of the cDNA encoding alternative splicing
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C; Keywords:
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C; Date: 20-Feb-1995 #sequence_revision
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N;Alternate names: GM-CSF receptor alpha-3 chain; hematopoietic growth factor
    A:Title: Cloning, expression, and mutational analysis A; Reference number: ISO455; MUID:94283267
A; Accession: ISO455
                                                                                                                                                                                                                                                                                                                                                             RESULT
IS0455
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A; Residues: 241-315,317-378
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                                                                                                                   Endocrinology 135,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   108 VQLQDPRE----PRRQATQMLKLQNLVIPWAPENLTLHKLS--ESQLELNWNNRFLNHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alternative splicing; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                       269-276, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INVSGDLENRYNFPSSEPRAKHSVKIRAADVRIL----NWSSWSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <WUH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 135.5; DB 2
Pred. No. 0.00082;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-Feb-1995
                                                                                                                                                                                                                                          13-Sep-1996 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----SCFIYNADLMNCTW-ARGPTAPRDV 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIDN: AAA60962.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      growth factor receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two
                                                                                  of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --- KKEIHLYOTFV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alternative splicing-derived
                                                                              pigeon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-Nov-1999
                                                                              prolactin receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-224; PSRBL/ <MO3>
A; Residues: 1-224; PSRBL/ <MO3>
A; Cross-references: GB:M27960; NID:g198365; PIDN:AAA39300.1; PID:g309409
A; Note: part of this sequence, including the amino end of the mature prote
A; Note: three forms of cDNA were isolated; the longest encodes extracellula
acellular domain and may encode a soluble form of the receptor
R; Harada, N.; Castle, B.E.; Gorman, D.M.; Itoh, N.; Schreurs, J.; Barrett,
Proc. Natl. Acad. Sci. U.S.A. 87, 857-861, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A:Title: The murine interleukin-4 receptor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 *sequence_revision 30-Jun-1993 *text_change 01-Dec-2000 C;Accession: A33380; B3380; 
A; Molecule type: DNA
A; Residues: 1-73,'1',75-333,'p',335-810 <RES>
A; Cross-references: GB:M64879; NID:g198359; P
                                                                                                                                                                                                                                                                       A;Cross-references: GB:M29854; NID:g198346; R;Wrighton, N.C.; Campbell, L.A.; Lee, F.D. Growth Factors 6, 103-118, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N; Alternate names: IL-4
C; Species: Mus musculum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              멍
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues; 1-830 <CHESA;Residues; 1-830 <CHESA
                                                                                                                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                        A; Title: The murine interleukin-4 receptor gene: A; Reference number: I54232; MUID:92265335 A; Accession: I54232
                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-810 <HAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Expression cloning of a cDNA encoding A; Reference number: A34861; MUID: 90138976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-258 < MO2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A34861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38 VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              D----IGEWSEWSSERH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WSPPPLADVTSNSHYYRYELRLKPEEKEEWETVSVGVQTQYKVNRLQAGVKYVVQVRCVL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WNNRFL-----NHCLEHLYQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRF 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KNHTNPWTTYNITYMAMNEIGSNSSDPQYVDVTSIVQPDAPVNLSLETKTSASTTYLLAK 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKEIHLYQTFVVQLQDPREPRRQAT--QMLKLQNLVIPWAPENLTLH---KLSESQLELN 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IRCRSLEKETFSCWWKPGSDGGLPTNYTL--FYSKDSEEKIYECPDYGMSG--PNSCYFD 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GB:M27959; NID:g198363; PIDN:AAA39299.1; PID:g309408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           receptor
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        PIDN: AAB59727.1;
                                                                                                                                                                                                                                                                                                                                                             PIDN: AAA39297.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the murine interleukin 4 receptor
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                                                                                                                                                                                                                                          Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96;
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C;Genetics:
A;Introns: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2
A;Introns: 24/1; 71/2; 122/1; 172/3; 225/1; 258/2; 284/3; 301/2
C;Superfamily: interleukin-4 receptor; cytokine receptor; plycoprotein; transmer; 1-25/Domain: signal sequence #status predicted <SIG>F; 26-810/Product: interleukin-4 receptor #status experimental <MAT>F; 26-23/Domain: extracellular #status predicted <EXT>F; 34-219/Domain: cytokine receptor homology <CRS>F; 324-257/Domain: transmembrane #status predicted <TMM>F; 258-810/Domain: intracellular #status predicted <INT>F; 258-810/Domain: intracellular #status predicted <Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y.
                                                                                                                                                                                                                                                                                                                                                                           A:(cross-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
Comment: Mouse high-affinity IL-5, GM-CSE, and one class of high-affinity IL-3
Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C:Keywords: cytokine receptor; duplication; transmembrane protein
F:1-22/Domain: signal sequence *status predicted <SIG>
F:23-896/Product: cytokine receptor common beta chain *status predicted <MAT>
F:23-896/Product: cytokine receptor bomology <CRSJ>
F:33-441/Domain: cytokine receptor homology <CRSJ>
F:33-235/Domain: cytokine receptor homology <CRSJ>
F:442-463/Domain: cytokine receptor homology <CRSJ>
F:442-463/Domain: iransmembrane *status predicted <TMM>
F:464-896/Domain: intracellular *status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule 4.... Acad. Sci. U.S.A. 87, 5459-5463, 1990
A; Title: Cloning and expression of a gene encoding an A; Reference number: A35782; MUID:90319131
A; Molecule 4...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δÃ
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                                                                                                                                                      В
                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine receptor common beta chain precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999 C;Paccession: A35782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-896 <GOR>
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Best Local
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                                                                                                                                                                                                          38 VQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQK 97
                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                         LQCFFDGIQSLHCSWEVWTQ-TTGSVSFGLFYRPSPVAPEEKCSPVV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NVTYKEPRLSFPINILMSGVYYTARVRVRSQILTGT---WSEWSPSITW 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SVDY---RHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPSGNVKPLAPDNLTLHTNVSDEWLLTWNNLYPSNNLLYKDLISMVNISREDNPAEFIVY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCL--EHLVQY----RTDWDHSWTEQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----RLMFFEFSENLTCIPRNSASTVCVCHMEMNRPVQSDRYQMELWAEHRQLWQGSF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNDKVQKCSHYLFSEEIT-----SGCQLQKKEIHLYQTFVVQLQDPREPRRQATQML 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TSVGCLILLLVTGSGSIKVLGEP--TCFSDYIRTSTCEWFLDSAVDCSSQLCLHY----
ESQLELNWNNR-----FLNHCLEHLVQYR---TDWDHSWTEQSVDYRHKFSLPSVDGQKR 196
                                                      KEPPGASVYTRYHCSLPVP-EPSAHSQYTVSVKHLEQGKFIMSYNHIQMEPPTLNLTKNR 355
                                                                                                     KE---IHLYQTFVVQLQDPREPRRQATQMLKLQNLV-----
                                                                                                                                                                                                                                                              48;
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                                                                                                                                                                                                                                                                                    9.7%;
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                                                                                                                                                                                                                                                        Score 125; DB 1;
Pred. No. 0.017;
6; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 132;
Pred. No. 0.
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5463, 1990
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                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                          Length 896;
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                                                                                                     ---IPWAPENLTLHKLS 144
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prolactin receptor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
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145971
                                                                              A;Molecule type: mRNA
A;Residues: 1-800 <RIC>
A;Cross-references: EMBL:X69903; NID:g56390; PIDN:CAA49528.1; PID:g56391
A;Cross-references: EMBL:X69903; NID:g56390; PIDN:CAA49528.1; PID:g56391
C;Superfamily: interleukin-4 receptor; cytokine receptor homology
C;Keywords: cytokine receptor
F;34-218/Domain: cytokine receptor homology <CRS>
                                                                                                                                                                                                                 R;Richter, G.; Hein, G.; Blankenstein, T.; Di
submitted to the EMBL Data Library, December
A;Reference number: S31575
A;Accession: S31575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992
A;Title: Molecular cloning of the bovine prolactin receptor and
A;Reference number: I45971; MUID:93246019
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                                                                                                                                                                                                                                                                                                   C; Accession:
                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
S31575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: PRLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:L02549; NID:g163617; PIDN:AAA51417.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-581 <SCO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I45971
                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                            interleukin-4 receptor - rat
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Best Local
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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197 YTFRVRSRFNPLCGSAQHWSEWSHPIHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                             173 KPEKATDWETHFTLKQTQLK-IFNL--YPGQK---YLVQIRCKPDHG---YWSEWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28 LSVSTL---PLPE----VQCFVFNVEYMNCTWNSSSE-PQPTNLTLHYWYKNSDNDKVQK 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QATQMLKLQN-----LVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CPDYK----TGGPNSCYFSKKHTSIWKMYVITVNAINQMGISSSDPLYVHVTYIVEPEP 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CSHYLFSEEITSG---CQLQKKEIHLYQTFVVQL-----QDPR-----EPRR 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSVSLLNGQSPPEKPKLVKCRSPGKETFTCWWEPGADGGLPTNYTLTY-HKEGET-LIHE 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 25.4 60; Conservative
  Similarity
                                                                                                                                                                                                                                                                                                     S31575
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  9.3%;
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25.4%; Pred. No. 0.02;
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    Pred.
                         Score
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                                                                                                                                                                                                                                                                 T.; Diamantstein, cember 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   224
  119.5; DB
No. 0.044;
                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69;
                     Length
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                           : 800;
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Matches

58;

Conservative

19;

Mismatches

, 88

Indels

53;

Gaps

Search completed: June 28, 2002, 07:42:52 Job time: 127 sec

Run

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tal number of hits satisfying chosen parameters:
        score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
                                                                                                                                                                                  853.5
853.5
207
207
207
207
199.5
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/iaa/Packfiles1.pep:*
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US-08-595-974-4
US-08-052-205-11
US-08-052-205-974-9
US-08-695-974-9
US-08-695-974-9
US-08-69-595-974-9
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US-08-952-217-115
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US-08-052-205-7
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Appli	7,	Sequence	US-08-442-281-7		332		115	5
Appli	•	Sequence	US-08-442-282-7	۲	332		115	44
Appli	•	Sequence	-390	ᆫ	332		115	3
Appli	-	Sequence	-727	ν	315		115	2
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Appli	•	Sequence	US-08-442-282-8	_	315		115	0
Appli	•	Sequence	US-07-757-390-8	_	315		115	39
Appli	-	Sequence	-939-727	N	415		118	38
Appli	•	Sequence	US-08-442-281-5	Н	415		118	37
Appli	-	Sequence	US-08-442-282-5	H	415		118	36
Appli	-	Sequence	US-07-757-390-5	ш	415		118	35
Appli	-	Sequence	-727	N	398		118	34
Appli	-	Sequence	US-08-442-281-6	ᆫ	398		118	3
Appli	-	Sequence	US-08-442-282-6	Н	398		118	2
Appli	-	Sequence	US-07-757-390-6	ᆫ	398		118	3
Appli	-	Sequence	US-08-421-823-3	_	335		118	30
Appli	ω,	Sequence	US-08-421-822-3		335		118	9
Appli	Ψ	Sequence	US-07-947-130-3	<u></u>	335		118	8

ALIGNMENTS

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; MOLECULE TYPE: protein US-08-052-205-7
                                                                                     REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-61
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08052205
Patent No. 5510259
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                               CLASSIFICATION: 435

PRIOR APPLICATION DATA:

PAPPLICATION NUMBER: JP 104947/1992

FILING DATE: 23-APR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Oblow, No. 5510259man F.
                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19930422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                         LENGTH:
TYPE: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1755 S. CITY: Arlington STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT, ADDRESSEE: P.C.
                                         TOPOLOGY:
                                                       AMINO ACID
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1755 S. Jefferson Davis Highway, Suite 400
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SHIMAMURA, TOSHIRO
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ASAO, HIRONOBU
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RESULT 2
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US-08-595-974-7
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Best Local Similarity 100.
Matches 232; Conservative
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                                                                               TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,974
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                       TELEPHONE: (703) 413-3000
                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5705608man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
            MOLECULE TYPE:
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ETILING DATE: 22-APR-1993
APPLICATION NUMBER: UP 104947/1992
FILLING DATE: 23-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1755 S.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
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                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 60
                                                                  LENGTH:
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                                                amino acid
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Y: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
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1755 S. Jefferson Davis Highway, Suite 400
                                                                  347 amino acids
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SHIMAMURA, TOSHIRO
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            protein
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                                                                                                                                                                                              10-615-0x
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Pred. No. 9.5e-119;
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RESULT 3
US-08-052-205-4
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; TOPOLOGY: li
; MOLECULE TYPE:
US-08-052-205-4
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
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Best Local
                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                   FILING DALL. 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
APPLICATION NUMBER: 23-APR-1992
TOTAL DATE: 23-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC -DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 369 amino acids
TYPE: AMINO ACID
                                                                                                                                                                               FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SUZUKI, MANABU
APPLICANT: HAMORO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                        TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: UP
FILING DATE: 19930422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Arlington
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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1755 S. Jefferson Davis Highway, Suite 400
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ASAO, HIRONOBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SHIMAMURA, TOSHIRO
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                                      linear
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                   protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 1288; DB 1; 100.0%; Pred. No. 9.5e-119;
                                                                                                                                                                                                                                                                                                                                                                                                      Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                    US/08/052,205
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                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25
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; MOLECULE TYPE: protein US-08-595-974-4
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US-08-595-974-4
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Best Local S
Matches 232
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                                                                                                      TELEFAX: (703) 413-222
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 1/30 CITY: Arlington STATE: Virginia
                                                                                                                                                                      FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, NO. 5705608man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SUGAMURA, KAZUO
APPLICANT: TAKESHITA, TOSHIKAZU
APPLICANT: ASAO, HIRONOBU
APPLICANT: NAKAMURA, MASATAKA
APPLICANT: SHIMAMURA, TOSHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
NUMBER OF SEQUENCES: 21
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                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
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                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/595,974 FILING DATE: 06-FEB-1996
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                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             83 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
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                                                                                                                                                         TELEPHONE:
                                                               LENGTH:
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5. 5705608
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                                              amino acid
                                                               369 amino acids
                                                                                                                                      (703) 413-3000
(703) 413-2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 1288; DB 1 llarity 100.0%; Pred. No..1e-118; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OBLON, SPIVAK, McCLELLAND, MAIER & NEUSTADT,
                                                                                                      4:
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; MOLECULE TYPE: US-08-052-205-11
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                                                TELERAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 230 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 11, App
Patent No. 5510
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                                                                                                                                                                                   APPLICATION NUMBER: US/08/052,205
APPLICATION UMBER: US/08/052,205
FILING DATE: 19330422
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
REGISTRATION NUMBER: 24,618
REGERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
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APPLICANT: SUGAMU
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 22202
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 254
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
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nes 232; Conserv
                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LNTTILTPNGNEDTTADFFLITMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arlington E: Virginia TRY: U.S.A.
                                                      AMINO ACID
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                                                                                                                                                     (703) 413-3000
(703) 413-2220
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SHIMAMURA, TOSHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASAO, HIRONOBU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAKESHITA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUGAMURA, KAZUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OBLON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                  protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 1288; DB 1; 100.0%; Pred. No. 1e-118; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPIVAK, McCLELLAND, MAIER & NEUSTADT
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US-08-595-974-11
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Best Local Similarity
Matches . 230; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                               TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-615-0X
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                                                                                                                                                                 FILING DATE: 23-APR-1992 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: |
FILING DATE: 22-APR-
APPLICATION NUMBER: |
                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                 MOLECULE
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AXILE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                LENGTH:
TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Virginia COUNTRY: U.S.A.
                                 TOPOLOGY:
                                                                                                                                                                                                                   NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: p.C.
STREET: 1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22202
                                             amino acid
                                                                                                                                                                                                                  Oblon, No. 5705608man F.
             TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/08595974
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TAKESHITA, TOSHI
ASAO, HIRONOBU
                                                                230 amino acids
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SHIMAMURA, TOSHIRO
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                                  linear
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                                                                                                                                                                                                                                                 UMBER: JP 104947/1992
23-APR-1992
                                                                                                                                                                                                                                                                                                                                                    06-FEB-1996
                                                                                                                                                                                                                                                                                    22-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MANABU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.1%; Score 1277; DB 1; 100.0%; Pred. No. 6.4e-118;
                                                                                                                                                                                                                                                                                                   US 08/052,205
                                                                                                                                                                                                                                                                                                                                                                                                     Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                    US/08/595,974
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US-08-052-205-9
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US-08-052-205-9
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APPLICANT: SUGAMUR
APPLICANT: TAKESHI
APPLICANT: ASAO, H
APPLICANT: NAKAMUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Patent No.
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Best Local Similarity
                                                                                                      TELEPHONE: (703) 413-300
TELEFAX: (703) 413-2220
TELEX: 24885 OPAT UR
INFORMATION FOR SEQ ID NO: 9
                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 2202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                       REFERENCE/DOCKET NUMBER: 10
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 413-3000
                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               APPLICATION NUMBER: JF 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5510259man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                TOPOLOGY: 1: MOLECULE TYPE:
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APPLICANT: HAMURO, JUNJI
TITLE OF INVENTION: HUMAN IL-2 RECEPTOR GAMMA CHAIN MOLECULE
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                                                    TYPE:
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                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arlington
                                                AMINO ACID
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Y: U.S.A.
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1755 S. Jefferson Davis Highway, Suite 400
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SHIMAMURA, TOSHIRO
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                                   linear
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                                                                                                                                                                                                                                                                                                                                                             US/08/052, 205
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US-08-595-974-9
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Sequence 9, App....
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Best Local :
                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/052,205
FILING DATE: 22-APR-1993
APPLICATION NUMBER: JP 104947/1992
FILING DATE: 23-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5705608man F.
                                                                                                  TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                    NAME: Oblon, No. 5705608man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 10-61:
TELECOMMUNICATION INFORMATION:
                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/595,974 FILING DATE: 06-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                TOPOLOGY:
                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08595974
                                                                 252 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASAO, HIRONOBU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMURO, JUNJI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAKAMURA, MASATAKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUZUKI, MANABU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHIMAMURA, TOSHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUGAMURA, KAZUO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT
                                                                                                                                                          (703) 413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.1%; Score 1277; DB 1; 100.0%; Pred. No. 7.3e-118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
                                                                                                                                                                                           10-615-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                              HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: MURINE
INDIVIDUAL ISOLATE:
US-08-424-224-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 230; Conserv
                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/121,43
ETILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERNCE/DOCKET NUMBER: 2026
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
                                                                                                                                                                                                                             TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM FC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 345
STREET: NEW YORK
CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 800 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS: LENGTH: 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSK 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    143 TQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSV 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23 LITTILTPIGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWISSSEPQP 82
                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LNTTILTPNGNEDTTADFFLITMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10154
                                                                                                                                                                     AMINO ACID
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                                                                                                                                                          UNKNOWN
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                                                                                                                     PROTEIN
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MURINE IL-2R
USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                         08/121,435
                                                  IL-2R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/08/424,224
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PCT-US94-02891-69
; Sequence 69, Application PC/TUS9402891
; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                  APPLICATION UNBER: PCT/US94/02891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION UNBER: 08/031,143
APPLICATION UNBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
APPLICATION NUMBER: 26,728
APPLICATION NUMBER: 26,728
REGISTRATION NUMBER: 26,728
REGISTRATION NUMBER: 2036-4061
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
                                                                                                                                                                              TELEX: 421792
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN APPLICANT: SERVICES
APPLICANT: OFFICE OF TECHNOLOGY TRANSFER, NATIONAL APPLICANT: INSTITUTES OF HEALTH, BOX OTT, BETHESDA, MARYLAND 20892 USA TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF TITLE OF INVENTION: XSCID
                                     HYPOTHETICAL: N
ORIGINAL SOURCE:
                                                                                                MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
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                                                    DESCRIPTION: PROTEIN
POTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 345 PARK AVE.
CITY: NEW YORK
STATE: NEW YORK
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ZIP: 10154
ORGANISM: MURINE INDIVIDUAL ISOLATE:
                                                                                                                         TOPOLOGY:
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                                                                                                                                                              LENGTH:
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                                                                                                                               AMINO ACID
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                                                                                                                         UNKNOWN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 66.3%; Score 853.5; DB 2 67.2%; Pred. No. 5.2e-76;
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  IL-2R
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                                                                                                                  ; MOLECULE TYPE: protein US-08-609-572-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08609572 Patent No. 5710023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 156; Conserv
                                     Best Local Similarity
                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                         TELEFAX: (617) 876-5851 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: BIOWID, SCOLT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 380 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Whitters, Matthew
APPLICANT: Wood, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204 NHEPRESLPSVDELKRYTERVRSRYNPICGSSQQWSKWSQPVHWGSHTVEEN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 DYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 QKLNLQNLVIPRAPENLTLSNLSESQLELRWKSRHIKERCLQYLVQYRSNRDRSWTELIV 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    122 QMLKLQNLVIPWAPENLTLHKLSESQLELNWNNRFL-NHCLEHLVQYRTDWDHSWTEQSV 180
                                                                                                                                                          LENGTH: 380 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24 SSKYLMSSANEDIKADLILTSTAPEHLSAPTLPLPEVQCFVFNIEYMNCTWNSSSEPQAT 83
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                 16.1%; Score 207; DB 1; ilarity 25.4%; Pred. No. 1.9e-12; Conservative 46; Mismatches 106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neben,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/609,572
                                                                                                                                                                                                                                                                                                                           GI5268
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                                                         Length 380;
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                   Indels
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                                                                                                      Query Match
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                                                                                                                                                                                                                                                            TELEFAX: (617) 876-58 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Whitters, Matthew
APPLICANT: WOOD, Clive
TITLE OF INVENTION: CYTOKINE RECEPTOR CHAIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
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APPLICANT: Neben, Tamlyn
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CTTY: Cambridge
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                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                             NAME: Brown, Scott A.
REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE:
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NGSE-VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSW-----KPGIGVLLDT 167
                                NGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP-----T 61
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87 CambridgePark Drive
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Fitz, Lori
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25.4%;
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                                                                                    Score 207; DB 4;
Pred. No. 1.9e-12;
                                                                     Mismatches
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                                                                                                  Length 380;
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US-08-846-340-4
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Best Local Similarity
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APPLICANT: Collin
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                                                                                                                                                                                                                                                                                                                                   NAME: BIOWN, SCOTT A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GIT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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APPLICATION NUMBER: US/08/846,340
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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62 NLTLHYWYKNSDNDKYQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPRE--PRRQ 119
                                                                                                                                                                                                                                                      TYPE:
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                                      NGSE-VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSW-----KPGIGVLLDT 167
                                                                       NGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQP-----T 61
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87 CambridgePark Drive
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25.4%;
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                                                                                                         Score 207; DB 4;
Pred. No. 1.9e-12;
6; Mismatches 106;
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NYNLFYWYEGLDH--ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRS 225

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120 ATQMLKLQNLVIPWAPENLTLHKLSESQLELNWN---NRFLNHCLEHLVQYRTDWDHSWT 176

SYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLV

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US-08-846-344-4
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Patent No. 6268480
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                                                                                                                                                                                                                                                              Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GI.
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Genetics Institute,
STREET: 87 CambridgePark Drive
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                                 120 ATQMLKLQNLVIPWAPENLTLHKLSESQLELNWN---NRFLNHCLEHLVQYRTDWDHSWT 176
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                                                                                               62 NLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPRE--PRRQ 119
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CLASSIFICATION:
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                                                                       NYNLFYWYEGLDH--ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRS
SYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLV 284
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amino acid
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(617) 876-5851
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Fitz, Lori
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                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 498-8224 TELEFAX: (617) 876-5851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Whitters, Matthew APPLICANT: Wood, Clive TITLE OF INVENTION: CYTOKINE NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
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                                                                                                                                                                84 LFSEEITSGCQLQKKEIHLYQTFVVQL--QDPREPRRQATQMLKLQNLVIPWAPENLTLH 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                             FRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                  VENSIDIRMKWSTPGGPIPPRCYTYEIVIRED-DISW-ESATDKNDMKLKRRANESEDLC 299
                                                                                                                                  LQHDEKNYGCKLSNLDSSDYKDFFICVNGSSKLEPIRSSYTVFQLQNIVKPLPPEFLHIS 241
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       Qyulay ......
QyzlaO cavia porce
QyzlaO cavia porce
QyzOk4 cavia porce
QyzOk5 yenopus lae
Qy7597 bos taurus
Q64146 rattus norv
Qyh573 homo sapien
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Q96bb4 homo sapien
Q951f1 canis famil
Q9hc73 homo sapien
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Q90xp8 oncorhynchu
Q951f0 canis famil
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Q9pti0 xenopus lae
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Matches 59
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID-8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYTOKINE RECEPTOR COMMON GAMMA CHAIN.
                                                                                                                                                                                                                                                                                           Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

MEDLINE=21287902; PubMed=11394690;

Wang T., Secombes C.J.;

Wang T. Secombes C.J.;

"Cloning and expression of a putative common cytokine receptor gamma "Chain gene in rainbow trout (Oncorhynchus mykiss).";

chain gene in rainbow trout (Oncorhynchus mykiss).";

Fish and Shellfish Immunol. 11:233-244(2001).

EMBL; AJ276623; CAC09429.2; -.
156 FLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGOKRYTFRVKSRFNPLCGSAQHW 215
                                                     80
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                                                                                                                                                  PEVQCFVFNVEYMNCTWNSSSEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQL 95
                                                    SYDKSDRFRTLKTKLV----HQNMSYVQDHNLKSMVKLYPPVNLSVEMNKDPELNLYWNNS 136
                                                                                      QKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWNNR 155
                                                                                                                           PNVNCLIINLDYVNCIWSEQSIPE-VNFT--FFSSRFIKDNMEECTTYLQEESYAVGCRL 79
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59; Conserv
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Pred. No. 3.7e~19;
7; Mismatches 88
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
01-DEC-2001 (RECEPTOR ALPHA-2.
TATERLEUKIN 13 RECEPTOR ALPHA-2.
                                                                                                                                                                                                                                                                                                                                                                                   Q95LFO;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
INTERLEUKIN 13 RECEPTOR ALPHA CHAIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Secombes C.J.; "Isolation and characterization of a putative interleukin 13 receptor alpha-Z sequence from rainbow trout (Oncorhynchus mykiss)."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AF361437; AAL26927.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q95LF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                            alpha2) cDNAs and tissues.";
                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=21287533; PubMed=11389954;
                                                                                                                                                                                                                                                                                                                                 Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                         IL13RA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lockyer A.E., Jones C.S., Noble L.R., Verspoor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=8022;
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                                                                    "Molecular cloning of canine IL-13 receptor alpha chain (alpha1 and alpha2) cDNAs and detection of corresponding mRNAs in canine
                                                                                                                            Tang L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               40 CFVFNVEYMNCTWNSS-SEPQPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQLQKK 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RGFWSDWS - - - HWSCHSDTES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EIHLYQTF--VVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNW---N 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEWSHPIHWGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             404 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20.1%; 27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 259.5; DB Pred. No. 9e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4B9B7E3F4CFFB6D6 CRC64;
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                                                                                                                                                                                                                                                                           Canis
                                                                                                                                                                                                                                                                                                         Euteleostomi;
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SDEGSLET-KIQDMKCIYYNWQYLVCSWKPGKTVYSDTNYTMFFWYEGLDH--ALQCADY 181

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RESULT
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                            Query Match
Best Local S
Matches 55
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Best Local Similarity
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01-NOV-1998
01-NOV-1998
01-DEC-2001
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SEQUENCE
                                                                                              Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-C3H/HEJ; TISSUE-THYMUS;
MEDLINE-98391042; PubMed-9725226;
Donaldson D.D., Whitters M.J., Fitz L., Neben T.Y.,
Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turner
Collins M.;
                                                                                                                                                                                     Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; U65747; AAC33240.1; -. EMBL, BC003723; AAH03723.1; -.
                                                                                                                                                                                                                                                                      "The murine IL-13 receptor alpha 2: molecular characterization, and comparison with murine J. Immunol. 161:2317-2324(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       088786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vet. Immunol. Ir EMBL; AF314533;
                                                                                                                      Interpro; IPR002996; CRIA.
Interpro; IPR003532; Hematopo_receptor_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN
                                                                                                                                                                                                                               Strausberg R
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                               MGD; MGI:1277954; Ill3ra2.
                                                                                                                                                                             HSSP; P16471; 1BP3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               176
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  25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TNLTLHYWYKNSDNDKVOKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDDPRE--PRR
TDSLSVSTLPLPEVQCFVFNVEYMNCTWN-SSSEPQPTNLTLHYWYKNSDNDKVQKCSHY 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTTTVENEIQITRTSNESQK-LCFLVRSKVNIYCSDDGIWSEWSDEQCWKGDIWKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TNYQLFYWYEGLDHS--AECTDYIKVNGKNMGCRFPYLESSDYKDFYICVNGSSESQPIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    V-1998 (TrEMBLrel. 08, Created)
V-1998 (TrEMBLrel. 08, Last sequence update)
V-2001 (TrEMBLrel. 19, Last annotation update)
RECEPTOR ALPHA 2 (INTERLEUKIN 13 RECEPTOR, ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61;
                             Similarity 25.7
55; Conservative
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                                                                                              383 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunopathol. 3; AAL14887.1;
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                                                                                               44482 MW;
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                                           15.5%;
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                              40;
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                             Score 199.5; DB 1
Pred. No. 4.7e-11;
0; Mismatches 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 213; DB 6;
Pred. No. 2.4e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A16FDF2DD023ED95 CRC64;
                                                                                               C25212325C47E35B CRC64;
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                                                                                                                                                                                                                                                                                                molecular cloning
                                                                                                                         UNKNOWN_1
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                                                        DB 11;
                              108;
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                                Indels
                                                                                                                                                                                                                                                                                                                        r K.J., Wood
                                                        Length
                                                                                                                                                                                                                                                                                    receptor alpha 1.";
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PARSULT QASSULT                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
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Best Local 9
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Q95LF1;
Q1-DEC-2001
Q1-DEC-2001
Q1-DEC-2001
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01-DEC-2001
01-DEC-2001
                                                                                                           Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.;
Submitted (OCT-2001) to the
EMBL; BC015768; AAH15768.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
INTERLEUKIN 13 RECEPTOR, ALPHA 1.
Tang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=COLON ADENOCARCINOMA;
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                                                                                                                                                                                                                  INTERLEUKIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                          Mammalia; Eutheria;
NCBI_TaxID-9615;
                                                                                                                                                                                              IL13RA1
                           MEDLINE=21287533;
                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFH---NDDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QLQKKEIHLYQTFVVQL--QDPREPRRQATQMLKLQNLVIPWAP--ENLTLHKLSESQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRVRSRFNPLCGSAQHWSEWSHPIHWGSNTSKEN 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLSESQLELNWN----NRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQHDEKNYGCKLSNLDSSDYKDFFICVNGSSKLEPIRSSYTVFQLQNIVKPLPPEFLHIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SVDGQKRYTFRVRSRFNPLC-GSAQHWSEWSHPIHWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LNWNN--RFLNHCLEHLVQYRTDWDHSWT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FFVRCKVNIYCADDGIWSEWSEEECWEGYTGPDS
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                                                                                                                                                                                                                (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
13 RECEPTOR ALPHA CHAIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AΑ;
                           PubMed=11389954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48676 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---FYEVEVNNSQTETHNVFYVQEAKCENPEFERNVENTSCFMVP
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26.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                              Craniata;
                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                     Fissipedia;
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                                                                                                                                            Vertebrata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4;
.2e-09;
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                                                                                                                        Canidae;
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                                                                                                                        Euteleostomi;
Canis.
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99HC733
1D 99HC733
1D 73PHC733
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9HC73;
Q9HC73;
Q1-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Receptor.
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CYTOKINE RECEPTOR CRL2 PRECUSOR (IL-XR) (THYMIC STROMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN RECEPTOR TSLPR). CRL2 OR IL-XR.
"Human thymic stromal lymphopoietin cells.";
J. Immunol. 167:336-343(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vet. Immunol.
                                                                                                          Reche P.A., Soumelis V. Johnston J., Liu Y.-J.,
                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=21311890;
                                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Tonozuka Y., Fujio Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                            monocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preferentially expressed
monocytes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhang W., Wang J., Wang Q., Zhang Y., Cao X.; "Identification of a novel description of a n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE=21134329; PubMed=11237741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                     Kastelein R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LNTTILTPNGNEDTTADFFLTTMPTDSLSVSTLP-----LPEVQCFVFNVEYMNCTW
                                                                                                                                                                                                                                                                                        Delta1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HLVQYRTDWDHSWTE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---IMVKDNARKIRPSFNIVPLTSHVKPDPPHIKRLF-FQNGNLYVQWKNPQNFYSRCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWNN--RFLNHCLE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPGRNTSPDTNYTLYYWH--SSLGKILQCED-IYREGQHIGCSFALTNLKDSSFEQHSVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NSSSEPQP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGCQL-----QKKEIHLYQ
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58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 Biophys.
                                                                                                                                                                                                                                                            (DEC-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Human).
Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunopathol.
2; AAL14886.1;
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                                                                                                                                                                          PubMed=11418668;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Res.
                                                                                                                                                                                                                                                                                                                K., Sugiyama T.,
of a human novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46328 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Commun.
                                                                                                                Spits
                                                                                                                                                                                                                                                            the
                                                                                                             Gorman D. Spits H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        y human dendritic cells an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     228
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                                                                                                                                                                                                                                                                                                                                                                                                                                    281:878-883(2001).
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                                                                                                                                         D.,
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                                                                                                                                                                                                                                                                                                                Nosaka T.,
type I cyto
                                                                                                                Menon S., Zurawski
e Waal-Malefyt R.,
                                                      preferentially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhang J., Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .9e-08
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                                                                                                                                                                                                                                                                                                                   cytokine
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                                                                                                                                                                                                                                                                                                                                               Hirai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CRC64;
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                                                            stimulates
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                                                                                                                                                                                                                                                                                                                      receptor
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                                                                                                                Bazan
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                                                                                                                                                                                                                                                                                                                                               Kitamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T.,
                                                                                                                J.F.,
                                                                                                                                                                                                                                                                                                                         related
                                                            myeloid
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                                                                                                                                                                                                                                                                                                                                            Τ.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    104
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Best Local S
Matches 51
                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 43
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SEQUENCE
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InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9UDY5
Q9UDY5;
Q9UDY5;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
INTERLEUKIN-13 RECEPTOR SOLUBLE FORM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00060;
SMART; SM00410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Wada M., Hisano T., Kuwano M.;
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ
EMBL; U81380; AAD00511.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hematopo_receptor_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
245
                                               150
                                                                                            188
                                                                                                                                                                                           131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202
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                                                                                                                     QLQKKEIHLYQTFVVQL--QDPREPRRQATQMLKLQNLVIPWAP--ENLTLHKLSESQLE 149
                                                                                                                                                                                                                           EVQCFVFNVEYMNCTWNSSSEPQP-TNLTLHYWYKNSDNDKVQKCSHYLFSEEITSGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVKAMEDVYGPDTYPSDWSEVTCW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLSESQLELNWNNRFLNHCLEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRV
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AB052639;
AF338733;
                                            LNWNN--RFLNHCLEHLVQYRTDWDHSWTE
                                                                                            DLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPPHIKNLSFH---NDDLY
                                                                                                                                                                                           ELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSL--EKIHQCEN-IFREGQYFGCSF 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RSR-FNPLCGSAQHWSEWSHPIHW 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -QKKETHLY------QTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLH 141
VQWENPQNFISRCL----FYEVEVNNSQTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51;
                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -TCSDLSYGD-----LLYEVQYRSPFDTEW-QSKQENTCNVTIEGLDAEKCYSFWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000282; Cytok_receptor_2.
IPR003961; FN_III.
IPR003600; Ig_like.
00060; FNS; 1.
00410; IG_like; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.4%;
nilarity 25.0%;
Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                       279 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             371 AA;
                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG27923.1;
BAB60717.1;
AAK60618.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42012 MW;
                                                                                                                                                                                                                                                                                                                                                                                                       31658 MW;
                                                                                                                                                                                                                                                                                                           11.0%;
28.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                    30;
                                                                                                                                                                                                                                                                               Score 141.5;
Pred. No. 1.2e
30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 159.5; DB Pred. No. 3.1e-07
Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 209
                                                                                                                                                                                                                                                                                                                                                                                                       E74141FE9F8E9EBB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEA53814758B69E4 CRC64;
270
                                            177
                                                                                                                                                                                                                                                                                                             .2e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
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Q9Z0K4;
Q1-MAY-1999
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Q9Z1A0;
01-MAY-1999
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Cavia porcellus (Guinea pig).
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SEQUENCE
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InterPro;
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"Guinea pig IL5 receptor bet
Submitted (MAR-1997) to the
EMBL; U94688; AAC77520.1; -.
HSSP; P40189; 1BQU.
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Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae;
MCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
INTERLEUKIN-5 RECEPTOR BETA CHAIN.
alpha cDNA.";
Submitted (APR-1996) to the EMBL; U55215; AAD09361.1; ...
InterPro; IPR002996; CR1A.
                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1999 (TREMBLEGI. 10, 01-MAY-1999 (TREMBLEGI. 10, 101-JUN-2001 (TREMBLEGI. 17, 11TERLEUKIN-5 RECEPTOR ALPHA
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                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                 Norris T.E.; "Cloning and Characterization
                                                                                                                                                                                                                                                            NCBI_TaxID=10141;
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                                                                                                                                                                                                  FROM N.A.
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Rodentia;
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Last annotation updat
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                                                                                                                                 of
                                                                                                                                                                                                                                                                                                  Hystricognathi;
                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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Mismatches
                                                                                                                                     the
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No. 7.9e-05;
                                                                                                                                 Guinea Pig Interleukin-5
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                                                                                                                                        receptor
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057519;
01-JUN-1998
01-JUN-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003529; Hematopo_receptor_L_F2.
Pfam; PF00041; fn3; 4.
SMART; SM00060; FN3; 1.
PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chen J., Grace A., Chien K.R.;

*Partial characterization of putative Xenopus Submitted (JAN-1998) to the EMBL/GenBank/DDBJ EMBL; AF041845; AAC03531.1; -.

#ISSP; P40189; 18QU.
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SEQUENCE
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Ver
Amphibia; Batrachia; Anura; Mesobatrachia;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003961; FN_III.
InterPro; IPR003532; Hematcopo_receptor_S_F2.
Pfam; PF00041; fn3; 1.
PROSTE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
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                                                                                                                          FFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNCTWNSSSEPQ-PTNLTL-HYWYKNSDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YQVEKTTT---NAFVSTTDGVSKYSIQVRAAVSPHCRAMGLWSKWSQPVYVG 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YWYKNSDNDKVQKCSHYLFSEEITS---GCQLQKKEIH--LYQTFVVQLQDPREPRRQAT 121
                                             KVQKCSHYLFSEEITSGCQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQ--NLVIPW 133
                                                                                                 FFTLGLPPDKPT-----NLTCIVYNQDNLTCTWDPGRPTNLPTNYTLSHRWAHFGAN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWSHPIHWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----QMLKLQNLVIPWAPENLTLHKLSESQLELNWN---NRFLNHCLEHLVQYRTDWDH
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                                                                                                                                                                                               51;
                                                                                                                                                                                                                      Similarity
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54; Conservative
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                                                                                                                                                                                                                                                                                                               881 AA;
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                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
-YCRGANNSCTIHSPGFQFYIDTTFQVEATNELGIQKSETLTIDPVNIVKPN
                                                                                                                                                                                                                                                                                                               HEMATOPO_REC_L_F2; UNKNOWN_1.
; 99003 MW; 7DE7942D211138A0 CRC64;
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46913 MW;
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23.3%;
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Last sequ
Last anno
                                                                                                                                                                                          Score 137.5; DB 13;
Pred. No. 0.00011;
1; Mismatches 94;
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Pred. No. 4.5e-05;
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INTERLEUKIN-5 RECEPTOR ALPHA
; 41BA4BA597B31CD4 CRC64;
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ia; Pipoidea; Pipidae;
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databases
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RESULT
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Best Local
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                                                                                      Q64146;
Q64146;
Q1-NOV-1996
Q1-NOV-1996
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Trigona W.L., Brown W.C., Estes D.M.;
"Functional implications for signaling via the bovine cells.";
Vet. Immunol. Immunopathol. 72:73-79(1999).
EMBL; AF074402; AAC98147.1;
InterPro; IPR003996; CRIA.
InterPro; IPR003532; Hematopo_receptor_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              O97597 PRELIMINARY; PRT; 349 AA. 097597, 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-DEC-2001 (TrEMBLrel. 19, Last annotation updat INTERLEUKIN-13 RECEPTOR ALPHA-1 CHAIN (FRAGMENT).
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SEQUENCE FROM N.A.

MEDLINE=20080132; PubMed=10614495;

Triqona W.L., Brown W.C., Estes D.M.;

Triqona W.L., Brown for signalin
            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammaalia; Eutheria; Rodentia;
                                                           RIL-3R<BETA>.
                                                                      01-NOV-1996 (TIEMBLIEL 01, Created)
01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-NOV-1996 (TIEMBLIEL 17, Last annotation update)
01-TOV-2001 (TIEMBLIEL) 17, Last annotation update)
INTERLEUKIN-3 RECEPTOR BETA-SUBUNIT (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bos taurus (Bovine).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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[1]
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                                                                                                                                                                                                                          TLNTVRIRVKTNKLCYEDDKLWSNWSQAMSIGQKANQ
                                                                                                                                                                                                                                               KRYTFRVRSRFNPLC-GSAQHWSEWSHPIHWGSNTSK 230
                                                                                                                                                                                                                                                                                                                                                                                                           IQCIWHNIRYMKCTWLPGRNASPDP---NYILYYWHNSL--GKILQCENFYREGQHIACS 152
                                                                                                                                                                                                                                                                                                                                                                                                                                       VQCFVFNVEYMNCTW----NSSSEPQPTNLTLHYWYKNSDNDKVQKCSH-YLFSEEITSG
                                                                                                                                                                                                                                                                                                                  NWNN--RFLNHCL----EHLVQYRTDWDHSWTE----QSVDYRHK-----FSLPSVDGQ
                                                                                                                                                                                                                                                                                                                                                 FNLTKVKDSSFEQHSVQVMVRDNAGKISPSFNIVPLTSHVKP-DPSHIKNLSFQNGDLYV
                                                                                                                                                                                                                                                                                     QWTNPQNFQSQCLCYEVEVINSHAETHDIFYVEEAKCQNTEFEGNLEGTICFMVPGVLPD
                                                                                                                                                                                                                                                                                                                                                                            CQLQKKEIHLYQTFVVQ---LQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SHRDSFTLQDLLPNTVYEVSIRCIHKDGHG---FWSDWS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52; Conserv
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349
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349
39644 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 137; DB 6;
Pred. No. 4.1e-05;
7; Mismatches 98;
                           Craniata; Vertebrata; Euteleostomi;
              Sciurognathi;
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                D61A4C918B1940A6 CRC64;
                                                                                                                                                   896
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              Muridae; Murinae;
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Best Local S
Matches 48
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-95370942; PubMed-7643220;
Appel K., Buttini M., Sauter A., Gebicke-Haerter P.J.;
"Cloning of rat interleukin-3 receptor beta-subunit fromicroglia and its mRNA expression in vivo.";
"J. Neurosci. 15:5800-5809(1995).
                                                                                                                                                                           בייים youa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID-9606;
                                                                                                                                                                                                                             Q9H5R3;
Q9H5R3;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA: FLJ23147 FIS, CLONE LNG09295.
Homo sapiens (Human).
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InterPro; IPR000282; Cytok_receptor_2.
InterPro; IPR003961; FN_III.
InterPro; IPR0033961; FN_III.
InterPro; IPR0033961; FN_III.
SMART; SM00060; FN3; 2.
                                                         Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ond Yamada K., Fujiwara T., Ond T., Suzuki Yamada K., Fujiwara Y., Suzuki Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
              "NEDO human cDNA sequencing Submitted (AUG-2000) to the EMBL: AK026800; BAB15557.1;
                                                                                                                                                                                                                                                                                                                            Q9H5R3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gebicke-Haerter P
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                                                                                                                                         TISSUE-LUNG;
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       418
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Local Similarity 23.9%;
tes 48; Conservative 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HCSLNVSDPAAHSQYTVSVK-----RLEQGKFIESFN-HIQMNPPTLNLTKNRDS-YSLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -CQLQKKEIHLYQTFVVQLQDPREPRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELN 151
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                             project.";
EMBL/GenBank/DDBJ
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 56946BE74C226FF5 CRC64
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RESULT
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Best Local
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MEDLINE=20289252; PubMed=10830440;
MEDLINE=20289252; PubMed=10830440;
Yamamoto T., Nakayama Y., Abe S.-I., Kawa
"Cloning of cDNA for Xenopus prolactin re
expression profile.";
Dev. Growth Differ. 42:167-174(2000).
EMBL; AB030443; BAA90400.1; -.
HSSP; P16471; 1BP3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9IBF6 PRELIMINARY;
Q9IBF6;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-DEC-2001 (TrEMBLrel. 1
PROLACTIN RECEPTOR.
                                                                                                                                                                                                                                                                                                                           InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN.III.
InterPro; IPR003528; Hematopo_receptor_L_F1
Pfam; PF00041; fn3; 1.
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoldea;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                 PROSITE;
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166
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les 55; Conserv
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                       LEHLVQYRTDWDHSWTEQSVDYRHKFSLPSVDGQKRYTFRVRSRFNPLCGSAQHWSEWS 219
                                                                           LQDPREPRRQATQMLKLQNLVIPWAPENLTLH-KLSESQLELNW-----NNRFLNHC
                                                                                                        LPTNYSL--LYRKENDPKIYECPDY-----VTSGLNSCFFDKAHTSFWIFYHIY----VN
                                                                                                                                  QPTNLTLHYWYKNSDNDKVQKCSHYLFSEEITSG----CQLQKKE-----IHLYQTFVVQ 109
                                                                                                                                                               NLAPTTP-----SVAVTFLLFLYTVSLNAQSLPGKPVIDKCRSYEKVTFSCWWKPGSDGG
                                                                                                                                                                              NTTILIPNGNEDITADFFLTIMPIDSLSVSTLPLPEV--QCFVFNVEYMNCTWNSSSE-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TCSDLSYGD-----LLYEVQYRSPFDTEWQTQSRSVTQAGVQWCDLCLLQPSPPR 185
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LKYEVRYKEEKEQEWEAHLVGNQLKLKLFGLTPGGNYVVQVRCK--PDSG---HWSEWS
                                                  ATNALGSNVSDEESVDTTYIVQPYPPTNVSLAVESGHHDLLLKWLPPAMVDVQSGWLT--
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                                                                                                                                                                                                                                                                                      611 AA;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                               Score 130; DB 13;
Pred. No. 0.00037;
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Pred. No. 3.2e-05;
3; Mismatches 54;
                                                                                                                                                                                                                                                                                      7E0DF76F21D8CE97 CRC64;
                                                                                                                                                                                                                     Mismatches
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Search completed: June 28, 2002, 07:44:30 Job time: 225 sec

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Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
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                                                                                                                                                                                                                                                                                                                                                                  and is derived
                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                             Score
                                                                    1195
1195
1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                                                                                                           Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A_Geneseq_032802:*

1: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1980.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1981.DAT:*

2: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:*

3: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

4: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1983.DAT:*

5: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1985.DAT:*

6: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1986.DAT:*

7: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*

9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*

9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*

9: /SIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1988.DAT:*
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                                                                                                                                                                                                                                                                                                                                                            is the number of results predicted by chance to have a ter than or equal to the score of the result being printed, ived by analysis of the total score distribution.
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111:
12:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    747574 seqs, 111073796 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-825-561A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                           SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
(SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA199.DAT: *
(SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *
(SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *
(SIDSI/gcgdata/hold-geneseq/geneseqp-embl/AA2000.DAT: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CPDLVCYTDYLQTVICILEM.....SDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                             Length
        289
5388
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                                                                                                                                                                                                                                                             DB
                                                                                                                                                                                                                                                             IJ
    AAB18634
AAY79312
AAY45031
AAY69886
AAB48001
AAB18629
AAY79316
AAY94304
                                                                                                                                                                           AAY69883
AAY27450
                                                                                                                                                                                                                 AAY45029
                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                             Human haemopoiétin
Human MU-1 hematop
A human zalphali 1
Human cytokine rec
Human Orphan Cytok
Human haemopoietin
Human II-9/II-2 re
                                                                                                                                                                                                                                                           Description
Amino acid sequenc
Maltose binding pr
Human HNOVILR poly
                                                                                                                                                                                                                 HUMAN Orphan Cytok
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12.1 894	144 12.1 842 18	12.1 805	12.1 783	12.1 539	12.1 878	12.1 600	12.1 600	12.1 596	2.1 592	12.1 576	12.4 878	14.7 57	14.7 57	14.7 57	14.7 57	14.7 57	14.7 57	30.3 237	33.5 397	3.6 144	45.5 144	45.9 158	70.1 529	70.6 529	90.1 568	90.1 568	90.1 568	95.2 375	95.8 460	97.0 538	1170 97.9 538 22	99.3 471	99.4
AAW24064	AAW22102	AAW22106	AAW24054	AAR06647	AAR78608	AAR92526	AAR78610	AAR78616	AAR92527	AAR78613	AAR92529	AAM32757	AAM19611	AAM72513	AAM59919	ABB24090	ABB39255	AAY69885	AAY79319	AAY69887	AAY69884	AAY69891	AAB48002	AAY79320	AAE02457	AAU08729	AAY94305	AAY69889	AAY69890	AAY69888	AAE02459	AAY45030	AAU08728
Murine WSX recepto	Murine leptin rece	Murine leptin rece	Murine WSX recepto	inter	Murine IL-3 recept	Fas antigen #1. S	Expression vector	Expression vector	Fas antigen #2. S	Expression vector	Fas sequence from	Peptide #6794 enco	Peptide #6045 enco	Human bone marrow	Human brain expres		Peptide #6761 enco	Human haemopoietin	Mouse cytokine rec	Mouse haemopoietin		Human NR8beta/FLAG		-	DNAX cyt	HNOVILR	Human HNOVILR poly	Human NR8alpha/TPO	Human NR8alpha/IgG		DNAX cyto	OCR10-Fo	Human HNOVILR poly

ALIGNMENTS

RESULT AAY45029

AAY45029 standard; Protein;

289 AA

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Region
                                                                                                                                             Peptide
                                                                                                                                                                                                   Human; Orphan Cytokine Receptor-10; OCR10; chromosome 16p12;
cytokine; screen; cognate ligand; treatment; endocrine disorder;
       WO200008152-A1.
                                                                       Domain
                                                                                        Domain
                                                                                                                            Protein
                                                                                                                                                        Key
                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                               HUMAN Orphan Cytokine Receptor-10 (OCR10) polypeptide
                                                                                                                                                                                                                                                   31-MAY-2000
                                                                                                                                                                                                                                                                     AAY45029;
                                           Region
                                                                                                                                                                                            disorder.
                                                                                                                                                                                                                                                   (first entry)
                                          /label= Transmembrane_domain
/note= "Putative and hydrophobic"
263.278
                                                                       /label= Proline_hinge_motif 238..255
                                                                                                           /label= mature_HUMAN_OCR10
118..169
                                                                                                                             /label= Signal_peptide
22..289
                         /label= Jak-binding_region
/note= "Potential"
                                                                                          122..123
                                                                                                /label= Proline_hinge_motif_region
                                                                                                                                                        Location/Qualifiers
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RESULT
AAY69883
ID AAY6
XX
AC AAY6
AC AAY6
AC AAY6
XX
DT 24-1
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Best Local S
Matches 218
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                                                                                      blood
                                                                                                Haemopoietin receptor family; NR8;
                                                                                                                                              24-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New HUMAN orphan cytokine receptors 10 and 10-A useful for drugs e.g. receptor agonists that may mediate survival differentiation in cells naturally expressing the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
               29-DEC-1999
                                      W09967290-A1
                                                              Homo sapiens
                                                                                                                                                                       AAY69883;
                                                                                                                                                                                            AAY69883 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-JUL-1999;
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                                                                                                                                                                                                                                                                                                    140
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mes 218; Conserv
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                                                                                                                                                                                                                                                                                                  sdyedpafymlkgklqyelqyrnrgdpwavsprrklisvdsrsvsllplefrkdssyelq
                                                                                                                                                                                                                                                      vragpmpgssyqgtwsewsdpvifqtqseelkegwnph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-205707/18.
                                                                                                                      haemopoietin receptor
                                                                                     formation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0128820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99WO-US16060
                                                                                      disorder
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                                                                                                                                                                                              Protein;
                                                                                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                              361
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                      family
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Pred. No. 6.4e-116;
                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                antibody; diagnosis;
                                                                                                                      member NR8alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Z
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                                                                                                                                                                                                                                                      237
                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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AAY27450
ID AAY2
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Matches 218
                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a novel haemopoietin receptor protein family NR8, designated NR8alpha. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                        cell proliferation; cytokine production; autoimmune disease; transplant rejection;
                                                                                                                                                     MU-1 hematopoietin receptor protein; e MU-1 protein; gene therapy; cell proliferation; cytokine production; immune response; cancer;
                                                                                                                                                                                Human MU-1 hematopoietin receptor protein.
                                                                                                                                                                                                       26-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders - \,
        (GEMY ) GENETICS INST INC
                                                17-MAR-1999;
                                                                     23-SEP-1999.
                                                                                         W09947675-A1
                                                                                                              Homo
                                                                                                                                                                                                                           AAY27450;
                                                                                                                                                                                                                                               AAY27450 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 5-6; 176pp; Japanese
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24-JUN-1998;
19-OCT-1998;
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                                                                                                                                                                                                                                                                                               sapiens.
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                                                                                                                                mapping;
                                                                                                                                                                                                                                                                                                                                                                                 tchmdvfhfmaddifsvnitdqsgnysqecgsfllaesikpappfnvtvtfsgqyniswr
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218; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maeda M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
llarity 100.0%;
Conservative 0
                                                                                                                                                                                                      (first entry)
                                                                                                                                 nutritional
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                             98US-0040005
                                                99WO-US05854
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98JP-0297409
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                                                                                                                                supplement;
                                                                                                                                                                                                                                               538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               score 1195;
Pred. No. 8.8
0; Mismatches
                                                                                                                                           rejection; hematopoiesis;
                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
3.8e-116;
es 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                           anemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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AAB18634
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
09-MAR-2000; 2000WO-US06067
                                                                                                                                                                                   zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma; tumourigenesis; leukaemia; hematopoiesis; B cell tumour.
                                                                                                                                                                                                                                                      A human zalphall ligand polypeptide
                                                                                                                                                                                                                                                                                                        22-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                  AAB18634 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This represents a MU-1 hematopoietin receptor protein. The protein can be produced by standard recombinant methodology. The MU-1 protein has the biological activity of the MU-1 hematopoietin receptor superfamily chain. It is used to screen for specific binding agents; to raise specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid encoding for treating e.g. cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
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                                            14-SEP-2000
                                                                                         WO200053761-A2
                                                                                                                                    Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 33-35; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              538
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                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1195; DB 20;
Pred. No. 1.6e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       218
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Best Local
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11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for cloning the zalphall gene. The zalphall ligand is useful for treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, agonists and antibodies are also useful for the detection, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a human zalphall ligand polypeptide, which is a cytokine. The zalphall ligand is useful for stimulating t proliferation and development of haematopoietic cells in vitro and i vivo. Zalphall ligand polynuclectides can be used as primers or prob
Cytokine receptor; zalphall; human; chromosome 16pll.1; apoptosis; signal transduction; growth factor; cancer; infection; immunosuppressive; immunostimulant; autoimmun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of haematopoietic cells in vitro and in vivo, and for treating tumourigenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OMYZ)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                               Human cytokine receptor zalphall.
                                                                                                                                 AAY79312;
                                                                                                                                                                AAY79312 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 255-256; 256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Johnston
                                                                                                  18-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevention, and treatment of diseases associated with a zalphall ligand
                                                                                                                                                                                                                                                               181 VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                140
                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                              vragpmpgssyggtwsewsdpvifqtqseelkegwnph 237
                                                                                                                                                                                                                                                                                                                sdyedpafymlkgklqyelqyrnrgdpwavsprrklisvdsrsvsllplefrkdssyelq
                                                                                                                                                                                                                                                                                                                             SDYEDPAFYMLKGKLQYELQYRNRGDPWAYSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                                                                                                                                                                                                                                                                                                                                                              TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                cpdlvcytdylqtvicilemwnlhpstltltwqdqyeelkdeatscslhrsahnathaty 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  defect.
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99US-0265992.
99US-0142013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑA;
                                                                                                                                                                  Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1195; DB 21; 100.0%; Pred. No. 1.6e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sprecher CA,
Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                  538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Foster DC, Hammond AK;
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 cancer; tur
autoimmune
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leukaemia; lymphoma; transplant rejection; therapy; diagnosis.

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cytokine receptor that may be involved in an apoptotic cellular capable of the provided in an apoptotic cellular capable of the provided provided proved in a provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provided provide
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stimulate
e.g. as a replacement for serum in culture media; in soluble form to block ligand activity (direct antagonists) and to detect ligand-expressing cancers; to raise specific antibodies; and for purification of cognate ligands. Agonistic ligands may stimulate cell-mediated immunity, e.g. for treating (viral) infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence is that of zalphall, a novel human class
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid encoding zalphall polypeptide, useful for treating e.g. viral infection or tumors, and for identifying ligands that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999;
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09-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAR-2000
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)B; AAZ94533, AJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27(e);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        infection or tumo:
cell proliferation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Page 148-149; 190pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0159254.
99US-0265117.
99US-0347930.
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20..237
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/note= "Box I signalling site"
301..304
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256..5
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238..2
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20..538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "intracellular signalling doma:
polypeptide comprising this do
specifically claimed in Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Box II signalling site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "transmembrane
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The present sequence is that of HUMAN Orphan Cytokine Receptor 10-A (OCRIO-A) polypeptide. It is expressed at high levels in spleen, thy peripheral blood leucocytes and lymph nodes and moderately in heart placenta. It has a role in immune system and cytokine function. It is

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                                                Example
                                                                              New HUMAN orphan cytokine receptors 10 and 10-A useful for drugs e.g. receptor agonists that may mediate survidifferentiation in cells naturally expressing the receptors.
                                                                                                                                   ; IAM
                                                                                                                                                                                                                                                                               Homo
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                                                                                                                                                                          (REGE-) REGENERON PHARM INC
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                                                                                                                                                                                                                                                                                                    cognate
                                                                                                                                                                                                                                                                                                            Human; Orphan Cytokine Receptor 10-A;
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1.6e-115;
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                                     This sequence represents a novel haemopoietin receptor protein family NR8, designated NR8gamma. Antibodies to the NR8 family proteins are ufor the diagnosis of blood formation disorders. Compounds identified binding to the proteins are used for the treatment of such disorders.
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Sequence
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19-OCT-1998;
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RESULT
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Best Local :
                                                                                                                                                                                                                                                                                             diagnosis
and in scr
The invention relates to isolated human and murine interleukin-9 (IL-9 /IL-2 receptor-like polypeptides. The plasmid containing the encoding cDNA insert is deposited as ATCC PTA-350. The IL-9/IL-2 receptor-like polypeptides (16445 proteins) can be recombinantly produced using standard recombinant methodology. The 16445 proteins are used for identifying their modulators and for diagnosis and treatment of immune inflammatory and respiratory disorders and disorders associated with lungs, colon, kidney and lymphoid tissues including tonsil and thymus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interleukin-9; IL-9;IL-2 receptor; 16445 protein; inflammatory;
T-lymphocyte-related disorder; antiarthritic; antipsoriatic; human;
immunosuppressive; antiasthmatic; antiallergic; antithyroid; cytostatic;
antidiarrheic; nephrotropic; gene therapy.
                                                                                                                                                                                                                                                                                                           Novel interleukin-9/interleukin-2 receptor-like polypeptides diagnosis and treatment immune, inflammatory and respiratory and in screening assays for identifying modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hodge
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DB; AAC84147.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MR
                                                                                                                                                                                                                                                                                             screening
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                                                                                                                                                                                                                                              Page 104-106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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20..538
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                                                                                                                                                                                                                                                                                             immune, inflammator identifying
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                                                                                                                                                                                                                                              English.
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11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in particular T-lymphocyte-related disorders including atopic conditions such as asthma, allergy, rheumatoid arthritis, psoriasis, chronic inflammatory diseases and graft verses host disease, disorders involving the colon such as diarrhoea, dysentery, infectious enterocolitis, kidney disorders including polycystic kidney disease, cystic renal dysplasia, disorders of the thymus including lymphomas, Hodgkin disease and carcinoids. The 16445 polypeptides are also useful as modulating agents in cellular processes including growth promoting activity, particularly the antigen-independent proliferation of T-helper cell clones. The encoding nucleic acid is useful as primers or hybridization probes for the detection of IL-9/IL-2 receptor-like encoding nucleic acids and for tissue typing and in forensic biology. The present sequence represents the human IL-9/IL-2 receptor-like polypeptide (AAH16445).
  New human cytokine,
                                      N-PSDB; AAA75609
                                                                                                                  Novak
                                                                                                                                                                                                                                                                       09-MAR-2000; 2000WO-US06067
                                                                                                                                                                                                                                                                                                                                              WO200053761-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                             zalphall ligand;
                                                                                              Johnston JV,
                                                                                                                                                                                                                                                                                                            14-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                      Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                          tumourigenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of MBP-human zalphall ligand fusion.
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                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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Similarity 100.0%;
18; Conservative 0;
                                                                                      Presnell SR, :
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                                                                                                                                                                                         99US-0264908.
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99US-0142013.
                                                                                                                                                                                                                                                                                                                                                                                                                                            cytokine;
leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein;
  designated
                                                                                            Sprecher CA,
Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                        haematopoietic cell proliferation; hematopoiesis; B cell tumour.
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Pred. No. 1.6e-115;
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zalphall ligand, useful for stimulating
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                                                                                            Foster
Hammond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytokine receptor; zalphall; maltose binding protein; human; apoptosis; signal transduction; growth factor; cancer; tumou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
and
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                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                     WO200017235-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection;
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                                                                                                                                                                                                                                                 "zalphall cytokine binding
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09-MAR-1999;
06-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
nephrotropic; hepatotropic; hypotensive; hypertensive; antifungal;
anti-HIV; antiprotozoal; antiviral; antianaemic; autoimmune disease;
Crohn's disease; Alzheimer's disease; Parkinson's disease; stroke;
                                              Human; anticancer; anti-inflammatory; immunosuppressive; antiallergic; antiasthmatic; antirheumatic, antiarthritic; nootropic; vasotropic; neuroprotective; antibacterial; cerebroprotective; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 13; Page 166-168; 190pp;
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                                                                                                                                                    08-AUG-2000
                                                                                                                                                                                                                      AAY94304
                                                                                                                 Human HNOVILR polypeptide
                                                                                                                                                                                                                                                                                                        569
                                                                                                                                                                                                                                                                                                                                      181
                                                                                                                                                                                                                                                                                                                                                                                                                                       449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l nucleic acid encoding zalphall viral infection or tumors, and
                                                                                                                                                                                                                                                                                                                      VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                                                                                                                                                                                                                                                                                                                    SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cpdlvcytdylqtvicilemwnlhpstltltwqdqyeelkdeatscslhrsahnathaty 448
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                                                                                                                                                                                                                                                                                                    vragpmpgssyggtwsewsdpvifgtgseelkegwnph 606
                                                                                                                                                                                                                                                                                                                                                                    sdyedpafymlkgklqyelqyrnrgdpwavsprrklisvdsrsvsllplefrkdssyelq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218;
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                                                                                                                                                                                                                      standard; Protein;
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99US-0265117.
99US-0347930.
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                                                                                                                                                                                                                      538
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1195; DB 21;
Pred. No. 1.9e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          polypeptide, useful for treating for identifying ligands that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hammond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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RESULT 1

AAU08728

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Best Local
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                                                                                                                                                                                                                                                                                    marrow using expressed sequence tag (EST) analysis. Alternatively it may be obtained from natural sources such as genomic DNA libraries or can be synthesised using commercially available techniques. The growth regulation and functional activities of cells are regulated through the interaction of cytokines and their cognate receptors. Thus the gene sequence and its product are useful for diagnosing or treating a wide range of diseases including cancer, inflammation, autoimmune disease, Crohn's disease, allergy, astema, rheumatoid arthritis, Alzheimer's disease, allergy, disease, multiple sclerosis, habed injury damage, septic shock, stroke, osteoporosis, osteoarthritis, cardiovascular disease, kidney disease, liver disease, ischemic injury, myocardial infarction, hypotension, hypertension, acquired immune deficiency syndrome (AIDS), male pattern baldness, and bacterial,
                                                                                                                                                                                                                                                                                                                                                                                                                                             multiple sclerosis; cancer; infection; cardiovascular disease.
                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-376497/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kikly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-NOV-1998;
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                                                                                                                                                                   H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             example cancer, inflammation, autoimmune disease
                                                                                                                                          VRAGPMPGSSYQGTWSEWSDPVIFQTQSEELKEGWNPH 218
                                                                                            SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KK,
vragpmpgssyggtwsewsdpvifqtqseelkegwnph
                                               sdyedpafymlkgklqyelqyrnrgdpwavsprrklisvdsrsvslhplefrkdssyelq
                                                                                                                                                                                           217;
                                                                                                                                                                                                                                                                            ncy syndrome (AIDS), protozoan and viral
                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        polypeptide of HNOVILR type used for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Michalovich
                                                                                                                                                                                                                                                     538
                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                     A
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                                                                                                                                                                                                       99.4%;
99.5%;
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                                                                                                                                                                                                                                                                             male patter
                                                                                                                                                                                          0;
                                                                                                                                                                                                      Score 1188;
Pred. No. 8
                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                      ; DB 21;
9.5e-115;
                                                                                                                                                                                                                  Length
                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or treating
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to human HNOVILR polynucleotides and polypeptides. The sequences can be used for diagnosing a disease or a susceptibility to a disease related to expression or activity of the polypeptide by determining the presence or absence of a mutation in the nucleotide sequence and/or analysing for the presence or amount of polypeptide expression in a sample derived from the subject. The HNOVILR polypeptides and polynucleotides are useful for screening to identify compounds that stimulate or inhibit the function of the polypeptide. These compounds the sequences of the invention can be used for treating or diagnosing cancer, inflammation (e.g. rheumatoid arthritis), autoimmunity, allergy, crohn's disease, Alzheimer's disease, Parkinson's disease, multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; HNOVILR; cancer; inflammation; rheumatoid arthritis; autoimmunity; allergy; Crohn's disease; Alzheimer's disease; Parkinson's disease; AIDS; multiple sclerosis; stroke; Sepsis; osteoporosis; ischaemia; hypotension; myocardial infarction; hypotrension; acquired immunodeficiency syndrome; fungal disease; bacterial disease; viral disease; cytostatic; nootropic; fungal disease; bacterial disease; viral disease; cytostatic; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         anti-inflammatory; immunosuppressive; antiallergic; neuroprotective; anti-Parkinsonian; cerebroprotective; antibacterial; osteopathic; vasotropic; cardiant; hypotensive; hypertensive; anti-HIV; gene therapy; human immunodeficiency virus; fungicide; antibacterial; virucide.
                                                                                                                                                                                                                                                                                                                                                                       infarction, hypotension, hypertension, acquired (AIDS), or fungal, bacterial or viral diseases. an HNOVILR polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 11-12; 17pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    osteoporosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New HNOVILR polypeptides and polynucleotides, useful for treating or diagnosing e.g. cancer, inflammation, autoimmunity, allergy, Alzheimer's disease, Parkinson's disease, multiple sclerosis, stroke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kikly KK, Michalovich
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       sclerosis, stroke,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MICH/) MICHALOVICH D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (KIKL/) KIKLY K K.
  121
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                                                                                                                                                    CPDLVCYTDYLQTVICILEMWNLHPSTLTLTWQDQYEELKDEATSCSLHRSAHNATHATY 60
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                                                                                                                                cpdlvcytdylqtvicilemwnlhpstltltwqdqyeelkdeatscslhrsahnathaty 79
SDYEDPAFYMLKGKLQYELQYRNRGDPWAVSPRRKLISVDSRSVSLLPLEFRKDSSYELQ 180
                                         TCHMDVFHFMADDIFSVNITDQSGNYSQECGSFLLAESIKPAPPFNVTVTFSGQYNISWR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-638508/73
                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                   538
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97EP-0309517
98US-0187711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ischaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                     sepsis, osteoporosis, ischaemia, myocardia
                                                                                                                                                                                                                                       99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ö
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                                                                                                                                                                                                                                       Score 1188;
Pred. No. 8
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                  18; DB 22;
8.5e-115;
ches 1;
                                                                                                                                                                                                                                                                                                                                                                                            immunodeficiency syndrome
This sequence represents
                                                                                                                                                                                                                                                            Length
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                                                                                                                                                                                                                                                                538;
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RESULT 1
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                                    The present sequence is that of HUMAN OCR10-Fc fusion protein, which is expressed as a soluble secreted protein. It comprises of extracellular domain from HUMAN OCR10 and crystallisable fragment (Fc) region of human immunoglobulin gamma-1 (IG21). HUMAN OCR10-Fc DNA insert can be used to tranform host cells or for studying efficacy of drugs for diseases associated with HUMAN OCR10 or OCR10-A polypeptide-mediated signal transduction. HUMAN Orphan Cytokine Receptor-10 (OCR10) gene is located on chromosome IGp12. It is expressed at high levels in spleen, thymus, peripheral blood leucocytes and lymph nodes and moderately in heart and placenta. It has a role in immune system and cytokine function. It is useful in screening for cognate ligands or drugs that mediate survival and differentiation of cells expressing this receptor. Modified HUMAN OCR10 or its agonist can be used in the treatment of endocrine or immune Aignates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; Orphan Cytokine Receptor-10; OCR10; chromosome 16p12; screen; cytokine; cognate ligand; endocrine disorder; immune HUMAN OCR10-Fc fusion protein; crystallisable fragment; Fc.
                                                                                                                                                                                                                                                                                                New HUMAN orphan cytokine receptors 10 and 10-A useful for drugs e.g. receptor agonists that may mediate survival differentiation in cells naturally expressing the receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY45030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY45030 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                          Masiakowski PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                     (REGE-) REGENERON PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200008152-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2000-205707/18
                               disorders.
                                                                                                                                                                                                                                                                                     for cognate ligands
                                                                                                                                                                                                                                                         Page 31-33; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                          Morris J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= Extracellular_domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Corresponds to HUMAN OCR10"
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                                                                                                                                                                                                                                                                                                                                  screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            treatment;
disorder;
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Query Match
Best Local Similarity
Matches 217; Conserv

Conservative

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Gaps

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99.3%;

Score 1187; DB 21; Pred. No. 8.9e-115; Mismatches

Length 471; Indels

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   SULT 14
E02459
                                                                                           WPI; 2001-343800/36.
N-PSDB; AAD06412.
                                                                                                                                                                                                                                                                                                                                                                                       Human; immunomodulator; DNAX cytokine receptor subunit 3.2; DCRS3.2; therapy; immunological disorder; drug screening; cell development; chromosome 16pl2; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-2001 (first entry)
The present sequence is human DNAX cytokine receptor subunit 3.2 (DCRS3.2) cDNA. DCRS3 gene is located on chromosome 16p12. Cytokine receptors, fragments and antibodies are useful for treating
                                     Claim 3; Page 16-17; 124pp; English.
                                                      New mammalian receptor proteins related to cytokine receptors, useful for regulating cell development and for diagnosis and treatment of immunological disorders -
                                                                                                                                       (SCHE ) SCHERING CORP
                                                                                                                                                           18-NOV-1999;
13-DEC-1999;
                                                                                                                                                                                    16-NOV-2000; 2000WO-US31363
                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                            Human DNAX cytokine receptor subunit 3.2 (DCRS3.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAE02459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAE02459 standard; Protein; 538 AA
                                                                                                                                                                                                                         WO200136467-A2
                                                                                                                                                                                                                                                                                                                                             Peptide
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99US-0170320
                                                                                                                                                                                                                                                                                      /note= "Human mature DNAX cytokine receptor subunit 3.2"
                                                                                                                                                                                                                                                    199
                                                                                                                                                                                                                                                                     /note= "Encoded by 136
                                                                                                                                                                                                                                          /note= "Encoded by CAN"
                                                                                                                                                                                                                                                                                                                    /label=
                                                                                                                                                                                                                                                                                                                                    /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                          note= "Encoded by ATN"
                                                                                                                                                                                                                                                                                                                   DCRS3.2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY69888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cc immunological disorders. DCRS3 (50R), DCRS4 (cytor) or fragments are cc useful in drug screening to identify compounds having binding affinity cc to the receptor subunit. Modulators of DCRS are useful for modulating cc the physiology or development of a cell or tissue culture cells. A cc purified DCRS is useful as a reagent to detect antibodies generated in cr response to the presence of elevated levels of expression, or cr immunological disorders which lead to production of antibody to the cendogenous receptor. Cytokine receptor sequences are useful as probes cc for detecting levels of the cytokine receptor in patients suspected of cc aving an immunological disorder. Antibodies have therapeutic value, are useful as potent antagonist, in detecting or quantifying ligands, for cc useful as potent antagonist, in detecting or quantifying ligands, for cc isolating DCRS proteins and peptides, to screen expression libraries for cc particular expression products, to raise anti-diotypic antibodies and cc for detecting or diagnosing various immunological conditions related to expression of the protein or cells which express the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                plood
                                                                                                                                                 24-JUN-1998;
19-OCT-1998;
                                          WPI; 2000-116933/10
N-PSDB; AAZ59242.
                                                                                                                                                                                                                                                       W09967290-A1
                                                                                                                                                                                                                                                                                                                               Haemopoietin receptor family; NR8; antibody; diagnosis;
                                                                                                                                                                                                                                                                                                                                                          Mouse haemopoietin receptor family member NR8gamma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY69888 standard; Protein; 538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                     Nomura H,
                                                                                                                    (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC
                                                                                                                                                                                            23-JUN-1999;
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                                                                                                                                                                                                                                                                                                                  formation
                                                                                     Maeda M;
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                                                                                                                                                98JP-0214720.
98JP-0297409.
                                                                                                                                                                                             99WO-JP03351
                                                                                                                                                                                                                                                                                                                  disorder.
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98.2%;
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Pred. No. 6.3e-113;
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Hemopoietin receptor protein family NR8 used for diagnosis of blood formation disorders -

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Search completed: June 28, 2002, 07:46:28 Job time: 343 sec
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                                                                                                                                                                                                                                                        Query Match 97.0%; Score 1159; DB 21; Length 538; Best Local Similarity 98.2%; Pred. No. 8.8e-112; Matches 214; Conservative 0; Mismatches 4; Indels 0;
                                                                                                                                                                                                                                                                                                                                              This sequence represents a mouse haemopoietin receptor protein family NR8, designated NR8gamma. Antibodies to the NR8 family proteins are used for the diagnosis of blood formation disorders. Compounds identified as binding to the proteins are used for the treatment of such disorders.
                                                                                                                                                                                                                                                                                                                       Sequence 538 AA;
                                                                                                                                                                                                                                                                                                                                                                                                            Claim 6; Page 152-158; 176pp; Japanese.
                                                          0; Gaps
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Run
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  850
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2: /SIDS1/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*

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Gapop 10.0 , Gapext 0.5
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519
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Homo sapiens W0200053761- 14-SEP-2000.	zalphall li tumourigene	human zai	2-JAN-2001	AAB18623;	T 1 623 AAB18623 SI		94.5 94.5	4	<u> .</u>		4.	4.	•					•		•		•			•	•	99.5	9.0	99.5
1s. L-A2.	gand; sis;	zalphall l	l (first		standard;		11.1 11.1	11.1	11.1	11.1	11.1	11.1	11.1	11.7	11.7	11.7 11.7		11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7	11.7
	cytokine; leukaemia;	ligand p	t entry)		Protein;		162 162	162	162	122	114	114	114	114	162	162 162	162	162	162	162	162	162	162	162	162	114	114	114	114
		ро1у	7				17 17	17	16	17	21	20	17	16	22	222	21	21	20	19	18	17	17	17	16	22	21) 19	17
	haematopoietic cell hematopoiesis; B ce	polypeptide.			162 AA.	ALIGNMENTS	AAW07254 AAR98526	AAW09100	AAR83436	AAR90842	AAY52311	AAY03759	AAW09101	AAR83309	AAB66397	AAB62012	AAY52308	AAB18632	AAY03756	AAW53878	AAW01658	AAR98527	AAW07255	AAW09098	AAR83438	AAB62013	0 (18	72
	<pre>:ll proliferation; lymphoma; cell tumour.</pre>						n epithelium n interleuki	Human epithelium d	interleu	Recombinant flag s	- m	Human epithelium-d	Human mature epith	Human 11-15. Homo Simian interleukin	interleu	Human interleukin Simian ETF (SETF)	Simian epithelium-	Amino acid sequenc	Simian epithelium-	3	Human interleukin-	Human interleukin- Wild-type interleu	Human epithelium-d	Simian epithelium	interleu		Mature simian epit	epithelium	Generic mammalian

Description A human zalphall 1 Amino acid sequenc A mouse zalphall 1 Amino acid sequenc Antigeninc peptide Antigeninc peptide Human Interleukin- Human interleukin- Mammalian interleu Mammalian interleukin-	XX PF XX PR XX PR I sequenc I sequen	XX PF XX PR XX PR I sequenc I sequen	XX PF XX PR XX PR I	XX PF XX PR IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
		2000WO-US060 99US-02649 99US-01420 99US-01420 3ENETICS INC. resnell SR, Nelson AJ, 5600/52.	2000WO-US06067. 99US-0264908. 99US-0265992. 99US-0142013. 3ENETICS INC. resnell SR, Sprecher CA, Nelson AJ, Dillon SR, S600/52. 5552.	2000WC-US06067. 99US-0264908. 99US-0265992. 99US-0142013. 3ENETICS INC. resnell SR, Sprecher CA, Foster DC, Nelson AJ, Dillon SR, Hammond AK, 5600/52.

useful for stimulating

Holly RD,

Gross JA;

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and
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                                                                                                                                                                                                                                                                                  zalphall ligand; cytokine;
tumourigenesis; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         vivo. Zalphall ligand polynucleotides can be used as primers for cloning the zalphall gene. The zalphall ligand is useful
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                                                                                                                                                                                                           WO200053761-A2
                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                              Amino acid sequence of MBP-human zalphall ligand fusion in pTAP126
                                                                                                                                                                                                                                                                                                                                                            22-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                      AAB18627
                                                                                       01-JUL-1999;
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                                                                                                                                                                              14-SEP-2000
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              Johnston
                                                        (ZYMO ) ZYMOGENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proliferation and/or development of haematopoietic cells in vitro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120
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            Presnell SR,
V, Nelson AJ,
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llarity 100.0%;
Conservative (
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99US-0265992.
99US-0142013.
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              Sprecher CA,
Dillon SR,
                                                                                                                                                                                                                                                                               haematopoietic cell proliferation; lymphoma; hematopoiesis; B cell tumour.
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Pred. No. 5.2e-87;
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               Foster
Hammond
               ₽C,
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Best Local :
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                           09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
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the plasmid pTAP126. Zalphall ligand is a cytokine. The zalphal
is useful for stimulating the proliferation and development of
haematopoietic cells in vitro and in vivo. Zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of haematopoietic cells in vitro and in vivo, and for treating tumourigenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 31; Page 233-235; 256pp; English.
                                                                                                                                                    WO200053761-A2
                                                                                                                                                                                                                zalphall ligand; cytokine; haematopoietic cell proliferation; lymphoma;
tumourigenesis; leukaemia; hematopoiesis; B cell tumour.
                                                                                                                                                                                                                                                           A mouse zalphall ligand polypeptide
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                                                                                                                                                                                                                                                                                                                        AAB18624;
                                                                                                                                                                                                                                                                                                                                                   AAB18624 standard; Protein;
                                                                                        09-MAR-2000; 2000WO-US06067
                                                                                                                      14-SEP-2000.
                                                                                                                                                                                 Mus musculus
                                                                                                                                                                                                              tumourigenesis;
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DB; AAA75599.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     defect.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                        (first entry)
                            99US-0264908.
99US-0265992.
99US-0142013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81.8%;
95.7%;
                                                                                                                                                                                                                                                                                                                                                      146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 695.5; DB 2
Pred. No. 4.6e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                      ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ligand fusion
The zalphall li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>ω</u>
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(ZYMO) ZYMOGENETICS INC

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RESULT
AAB18628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vivo. Zalphall ligand polynucleotides can be used as primers or probes for cloning the zalphall gene. The zalphall ligand is useful for treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a mouse zalphall ligand polypeptide, which is a cytokine. The zalphall ligand is useful for stimulating t proliferation and development of haematopoietic cells in vitro and i
                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                    zalphall ligand;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB18628 standard; Protein; 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prevention, and genetic defect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human cytokine, designated zalphall ligand, useful for stimulating the proliferation and/or development of haematopoietic cells in vitro and in vivo, and for treating tumourigenesis -
09-MAR-1999;
                                        09-MAR-2000; 2000WO-US06067
                                                                                      14-SEP-2000
                                                                                                                                    WO200053761-A2
                                                                                                                                                                                                                                                   tumourigenesis;
                                                                                                                                                                                                                                                                                                                      Amino
                                                                                                                                                                                                                                                                                                                                                                  22-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Johnston
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 yekrtpkeflerlkwllqkmihqhls 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 YEKKPPKEFLERFKSLLQKMIHQHLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 kghcehaafacfqkaklkpsnpgnnktfiidlvaqlrrrlparrggkkqkhiakcpscds 120
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                                                                                                                                                                                                                                                                                                                  acid sequence of MBP-mouse zalphall ligand fusion in pTAP134.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
92; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JV, Nelson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and treatment of diseases associated with a zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 222-223;
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΑĄ,
                                                                                                                                                                                                                                                cytokine;
leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57.2%;
63.0%;
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Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     256pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                                haematopoietic hematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 486; DB 21;
Pred. No. 2.4e-46;
3; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153
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                                                                                                                                                                                                                                                                    proliferation; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotides can be used as primers or probes for cloning the zalphall gene. The zalphall ligand is useful for treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for treating leukaemias and lymphomas. Antagonists against zalphall ligand are useful as research reagents for characterizing ligand-receptor interaction. Antagonists are also useful for inhibiting expansion, proliferation, activation and differentiation of cells involved in regulating hematopoiesis. The zalphall ligand may also be used to stimulate an immune response against B cell tumour, a virus, a parasite or a bacterium. The zalphall polypeptides, polynucleotides, antagonists, aganists and antibodies are also useful for the detection, diagnosis, aganists and antibodies are also useful for the detection, diagnosis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a MBP-mouse zalphall ligand fusion in the plasmid pTAP126. Zalphall ligand is a cytokine. The zalphall ligand is useful for stimulating the proliferation and development of haematopoietic cells in vitro and in vivo. Zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human cytokine, designated zalphall ligand, useful the proliferation and/or development of haematopoietic and in vivo, and for treating tumourigenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-MAR-1999;
01-JUL-1999;
                                                                                                       zalphall ligand; cytokine;
                                                                                                                                                                    22-JAN-2001
                                                                                                                                                                                                 AAB18625;
                                                                                                                                                                                                                              AAB18625 standard; Peptide; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic defect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 31; Page 239-240;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Johnston JV,
                                                                                        tumourigenesis;
                                                                                                                                    Antigeninc peptide derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ZYMO ) ZYMOGENETICS INC
                                                          domo sapiens
                                                                                                                                                                                                                                                                                                        510
                                                                                                                                                                                                                                                                                                                                    153
                                                                                                                                                                                                                                                                                                                                                                                                                                390
                                                                                                                                                                                                                                                                                                                                                                 450 ktfiidlvaqlrrrlparrggkkqkhiakcpscdsyekrtpkeflerlkwllqkmihqhl
                                                                                                                                                                                                                                                                                                                                                                                 33 DRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNN 92
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                                                                                                                                                                                                                                                                                                                                     S 153
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                                                                                                                                                                                                                                                                                                        510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 75; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       510
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V, Nelson AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and treatment of diseases associated with a zalphall
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0265992.
99US-0142013.
                                                                                          leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        46.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sprecher CA,
Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             256pp;
                                                                                        hematopoiesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                        haematopoietic cell proliferation; lymphoma; hematopoiesis; B cell tumour.
                                                                                                                                    from a human zalphall ligand polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 394; DB 21;
Pred. No. 2.5e-35;
o. Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                English.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Foster DC,
Hammond AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 510;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Holly RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            for stimulating cells in vitro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gross JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                449
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      PRR PR XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence was used to raise antibodies, and is derived from a human zalphall ligand polypeptide. Zalphall ligand is a cytokine. The zalphall ligand is useful for stimulating the proliferation and convergence of the calphall ligand is useful for stimulating the proliferation and convergence of the calphall ligand is useful in vitro and in vivo. Zalphall convergence of the calphall ligand saporin fusion toxin may be used for cloning the calphall ligand-saporin fusion toxin may be used for treating the convergence of the convergence of the convergence of the calphall ligand saporing the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the convergence of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 24.9%;
Best Local Similarity 100.0%;
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1999;
11-MAR-1999;
01-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevention, and treatment genetic defect.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New
                                                                                                                                                                                                                                zalphall ligand; cytokine;
tumourigenesis; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                   AAB18626 standard; Peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novak JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-MAR-2000;
09-MAR-1999;
11-MAR-1999;
                                                                09-MAR-2000; 2000WO-US06067
                                                                                                         14-SEP-2000
                                                                                                                                                WO200053761-A2
                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                               Antigeninc
                                                                                                                                                                                                                                                                                                                                     22-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                              AAB18626;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human cytokine, designated zalphall ligand, useful proliferation and/or development of haematopoietic in vivo, and for treating tumourigenesis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         qdrhmirmrqlidivdqlknyvndlvpeflpapedvetnc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ,VĽ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Presnell SR,
V, Nelson AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                            peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000WO-US06067
                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0264908.
99US-0265992.
99US-0142013.
    99US-0264908
99US-0265992
                                                                                                                                                                                                                                                                                               derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sprecher CA,
Dillon SR,
                                                                                                                                                                                                                                  haematopoietic cell proliferation; lymphoma; hematopoiesis; B cell tumour.
                                                                                                                                                                                                                                                                                            from a human zalphall ligand polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                          32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 212; DB 21; Pred. No. 2e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                       ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hammond
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Foster DC,
lammond AK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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WPI; 2000-022283/02

Bennett CF, (ISIS-) ISIS 25-NOV-1998; 25-NOV-1998; 16-NOV-1999 US5985663-A. Homo sapiens

Cowsert LM; PHARM INC

98US-0200141 98US-0200141. human;

infection; inflammation; tumour;

therapy; diagnosis

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RESULT
AAY54825
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Best Local Similarity
Watches 32; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence was used to raise antibodies, and is derived from the present sequence was used to raise antibodies, and is derived from the human zalphall ligand polypeptide. Zalphall ligand is a cytokine. CC The zalphall ligand is useful for stimulating the proliferation and development of haematopoletic cells in vitro and in vivo. Zalphall CC ligand polynucleotides can be used as primers or probes for cloning the CC zalphall gene. The zalphall ligand is useful for treating tumourigenesis. A zalphall ligand-saporin fusion toxin may be used for treating cC leukaemias and lymphomas. Antagonists against zalphall ligand are cuseful as research reagents for characterizing ligand-receptor cC interaction. Antagonists for characterizing ligand-receptor cC interaction, activation and differentiation of cells involved in cc regulating hematopoiesis. The zalphall ligand may also be used to cor a bacterium. The zalphall polypeptides, polynucleotides, antagonists, agonists and antibodies are also useful for the detection, diagnosis, prevention, and treatment of diseases associated with a zalphall ligand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Interleukin-15 protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 CPSCDSYEKKPPKEFLERFKSLLQKMIHQHLS 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-565600/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein; 135 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0142013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IL-15; antisense inhibitor; untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.7%; Score 176;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sprecher CA,
Dillon SR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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Hammond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 32;
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RESULT
AAR83310
ID AAR8
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AC AAR8
XY
DT 02-F
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KW Inte
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of having or being prone to a disease associated with IL-15 expression, e.g. infections, inflammation or tumours. The inhibitors can also be used for research or diagnostic purposes. Using antisense compounds specifically and effectively inhibits IL-15 function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This sequence is the human interleukin-15. The invention relates to antisense compounds that are targeted to a 5' or 3' untranslated region (5'UTR or 3'UTR) of a nucleic acid molecule encoding human interleukin-15 (IL-15), and inhibit the expression of human IL-15. The antisense inhibitors are is useful for inhibiting expression of IL-15 in human cells or tissues in vitro, for treating humans or other animals suspected
                                                                      Isolated DNA encoding polypeptide with mammalian II-15 activity - stimulates proliferation and differentiation of T cells, used for treating carcinoma(s), melanomas, etc. and viral infections
                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                       06-APR-1994;
                                                                                                                                                                                                                                                                                   06-APR-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antisense compound useful for inhibiting human interleukin-15 expression useful for treating diseases associated with interleukin-15
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                                            Claim 23; Page 30; 48pp; English.
                                                                                                                                                                               Anderson DM,
Rauch C;
                                                                                                                                                                                                                                                                                                                 19-0CT-1995
                                                                                                                                                                                                                                                                                                                                            W09527722-A
                                                                                                                                                                                                                                                                                                                                                                                                      Interleukin-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human interleukin-15 mature polypeptide
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                                                                                                                                                  WPI; 1995-373556/48.
                                                                                                                                                                                                                           (IMMV ) IMMUNEX CORP
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                                                                                                                                    AAT00527
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species of IL-15 (sIL-15) was purified and its AA and cDNA sequence analysed (see AAR83309, AAR83436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                           Eisenman
                                                                                                                                                                                                                                                       94WO-US03793
                                                                                                                                                                                                                                                                                   94WO-US03793
                                                                                                                                                                                                                                                                                                                                                                                                     epithelium-derived T-cell factor; T lymphocyte
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26.7%;
                                                                                                                                                                                             JR,
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Isolated DNA encoding polypeptide with mammalian II-15 activity - which stimulates proliferation and differentiation of T cells, used for treating carcinoma(s), melanomas, etc. and viral infections
                                                                             Anderson DM,
Rauch C;
                                                                                                                                          06-APR-1994;
                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR83435;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR83435 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT00524, AAT00525). Both the simian and the human ORFs encode a precursor polypeptide (AAR83436, AAR8348). The precursor polypeptides each comprise a 48-AA leader sequence and a sequence encoding mature simian or human IL-15 polypeptides. The active simian and human IL-15 polypeptides are disclosed in AAR83309 & AAR83310 respectively. The invention also comprises other mammalian IL-15, including human IL-15, that hybridise to probes defined by AAR83438. A plasmid contg. a recombinant clone of human IL-15 CDNA was deposited with ATCC on Feb. 19 193 under ATCC 69245. The deposit was named 141-hETF. AAR83435 is a mammalian mature IL-15 polypeptide. It is a generic sequence which encompasses both AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
                                                                                                                  (IMMV ) IMMUNEX CORP.
                                                                                                                                                                   06-APR-1994;
                                                                                                                                                                                             19-OCT-1995.
                                                                                                                                                                                                                      WO9527722-A.
                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                       Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalian interleukin-15 mature polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 tvenlii--lannslssngnvtes---gckeceeleeknikeflqsfvhivqmfin 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vnvisdlkk-iedligsmhidatlytesdvhpsckvtamkcfllelgvislesgdasihd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                         Eisenman
                                                                                                                                                                                                                                                                                                                                     /label= L,H
: 57
                                                                                                                                            94WO-US03793
                                                                                                                                                                     94WO-US03793
                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                               epithelium-derived T-cell factor; T lymphocyte
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                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                         /label=
                                                                                                                                                                                                                                                                        'label= S,I
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25.9%;
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                                                                                        Fung
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Pred. No. 0.0031;
                                                                                         ۲,
                                                                                         Grabstein
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RESULT RESULT AAR6692 AAR6692 AAR6 AC AAR6 XX AAR6 XX O4-S XX Interview of the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the two and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A simian species of IL-15 (sIL-15) was purified and its AA sequence and cDNA sequence analysed (see AAR83309, AAR83436, AAT00524, AAT00525). Both the simian and the human ORPs encode a precursor polypeptide (AAR83436, AAR83438). The precursor polypeptides each comprise a 48-AA leader sequence and a sequence encoding mature simian or human IL-15 polypeptides. The active simian and human IL-15 polypeptides are disclosed in AAR83309 sequence simian and human IL-15 polypeptides are disclosed in AAR83309 sequence simian and human IL-15, that hybridise to probes defined by AAR83310 respectively. The invention also comprises other mammalian IL-15; including human IL-15, that hybridise to probes defined by AAR8348. A plasmid contg. a recombinant clone of human IL-15 cDNA was deposited with ATCC on Feb. 19 1993 under ATCC 69245. The deposit was named 141-hETF. AAR83435 is a mammalian mature IL-15 polypeptide. It is a generic sequence which encompasses both AAR83309 (simian) and AAR83310 (human) IL-15 mature polypeptides.
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antitumor; virucide.
                                                                                                                                    18-APR-1994;
                                                                                                                                                                                   18-APR-1994;
                                                                                                                                                                                                                                         28-DEC-1994
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                                                                           (IMMV ) IMMUNEX CORP
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                      Fung
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                            ۲,
                         Grabstein KH;
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AAW09099
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Best Local
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08-MAR-1993;
22-APR-1994;
                                                                                                                                                                                                                                                                                         Key
Protein
                                                                                                                                                                                                                                                                                                                                               sETF; African green monkey; CV1/EBNA cell; T-cell; B-cell;
lymphocyte; proliferation; differentiation; gastrointestinal;
HIV infection; human immunodeficiency virus.
                 New epithelium derived T cell factor - induces proliferation of T and B cells, stimulates destruction of tumour and virus-infected cells and protects against toxicity, partic. for treating intestinal disease and HIV infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simian and human II-15 cDNAs (AAQ84583-84) can be used to obtain cDNAs encoding other mammalian homologs of II-15. A general sequence of mammalian II-15 is claimed.
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                                                                                                                                                                                                             08-MAR-1993;
                                                                                                                                                                                                                                                                                                                           Cercopithecus aethiops
                                                                                                                                                                                                                                                                                                                                                                                           Simian mature
                                                                          WPI; 1996-517923/51.
N-PSDB; AAT49455.
                                                                                                           Rauch
                                                                                                                                                                                                                                                        US5574138-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                          Anderson DM, Rauch C;
                                                                                                                                          (IMMV ) IMMUNEX CORP
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93US-0031399.
94US-0233606.
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                                                                                                                     JR,
                                                                                                                                                                                                                                                                                                                                                                                           derived T cell factor
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                                                                                                                     Fung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 99.5; DB 16; Pred. No. 0.0031;
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                                                                                                                       Grabstein
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Claim 1; Fig 1; 35pp; English

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RESULT 1
AAW07253
ID AAW07253
ID AAW0
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AC AAW0
AC AAW0
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epithelial
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New isolated simian and human epit which stimulate the proliferation T-lymphocytes and T-cell lines
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                                                                                                   WPI; 1996-412063/41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43 IDIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94 RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epithelium-derived T-cell factor; simian; human; culture; cell; proliferation; differentiation; T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                Eisenman J,
                                                                                                                                                                                                                                              9305-0031399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Ser,
                                                                                                                                                                                                                                                                                                93US-0031399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80
                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Val, Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= Ala,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ′label= Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epithelium-derived T cell factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein; 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11.7%;
25.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ser,
                                                                                                                                                Fung
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Asp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               His
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 99.5;
Pred. No. 0.
                       epithelium-derived T-cell factors tion and/or differentiation of
                                                                                                                                                ۷,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                  Grabstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                Rauch
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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RESULT :
AAW39186
ID AAW:
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Best Local
                                                                                                                     Anderson Rauch C;
                                                                                                                                                                               22-FEB-1995;
08-MAR-1993;
22-APR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This is the amino acid sequence of a generic mammalian epithelium-derived T cell factor (ETT). The pref. ETT are the simian (AAW07254) or human (AAW07255) proteins. This sequence represents the generic sequence of the mature protein. Both the human and simian proteins contain a 48 amino acid leader sequence. ETF is a protein of 15-17 kD which is expressed by epithelial cells and stimulates proliferation and/or differentiation of precursor and/or mature T cells. The protein is therefore useful for promoting long term in vivo culture of T-lymphocytes and T-cell lines.
                    Claim 1a; Column 37-38; 34pp; English.
                                            Treatment or prevention of gastrointestinal diadministering epithelium-derived T-cell factor
                                                                                 WPI; 1998-100295/09.
N-PSDB; AAV02873.
                                                                                                                                                                                                                                 04-OCT-1996;
                                                                                                                                                                                                                                                                                 US5707616-A.
                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                        Simian
                                                                                                                                                                                                                                                                                                                                                                                        B-cell stimulation; epithelium;
                                                                                                                                                                                                                                                                                                                                                                                                    Epithelium derived T-cell factor; ETF;
                                                                                                                                                                                                                                                                                                                                                                                                                             Simian epithelium derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW39186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW39186 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Column 29;
                                                                                                                                                       (IMMV ) IMMUNEX CORP.
                                                                                                                                                                                                                                                        13-JAN-1998
                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                               treatment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 tvenlillannxlssngnxtesg-----ckeceeleeknikeflqsfvhivqmfin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93 -- ERIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
30; Conserv
                                                                                                                              DM,
                                                                                                                                                                                                                                                                                                                                                                               prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                 Eisenman
                                                                                                                                                                                95US-0393305.
93US-0031399.
94US-0233606.
                                                                                                                                                                                                                                 96US-0726817
                                                                                                                                                                                                                                                                                                        /label=
                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
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                                                                                                                                 JR,
                                                                                                                                                                                                                                                                                                        ETF
                                                                                                                                                                                                                                                                                                                                                                                                                             T-cell factor mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114
                                                                                                                                 Fung V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 99.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                           villi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                 Grabstein KH;
                                                                                                                                                                                                                                                                                                                                                                                          simian; gastrointestinal disease
CD4+; CD8+; T-cell stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .0031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 17;
                                           diseases – by
tor polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5
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This sequence represents a simian epithelium-derived T-cell factor (ETF)

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RESULT7

AAYO3757

ID AAYY

AC AAYY

AC AAYY

AC AAYY

C AAYY

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Best Local S
Matches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-FEB-1995;
08-MAR-1993;
22-APR-1994;
04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mature protein which is used in a method for treating or preventing gastrointestinal disease. These polypeptides have particular application in the treatment of gastrointestinal disorders associated with disruption of the gastrointestinal epithelium or villi such as chemotherapy and radiation-therapy induced enteritis (gut toxicity), mucositis, peptic ulcer disease, gastroenteritis and colitis, villus atrophic disorders, malignancy and inflammatory bowel disease. ETF polypeptides may also be useful in the treatment of human immunodeficiency virus (HIV) and HIV-associated disease due to their ability to stimulate CD4+ and CD8+cells. Biologically active ETF may be used to treat a variety of other diseases or conditions where T-cell or B cell stimulation is desired.
The invention relates to an isolated antibody that binds specifically to a similar or human epithelium-derived T-cell factor (ETF) polypeptide. The antibodies are used, optionally when immobilized or labeled, to detect and quantify ETF in standard immunoassays. They may also be used as diagnostic and therapeutic agents, e.g. when conjugated to toxins (or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T cell proliferation; gastrointestinal disease; mucositis; colitis; gastroenteritis; villus atrophy; malignancy; inflammatory bowel disease; human immune deficiency virus; tumour; simian.
                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                             Anderson DM, Rauch C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-APR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Simian epithelium-derived T-cell factor (ETF) mature protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                              Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY03757 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43 IDIVDQLKNYVNDLVPEF----LPAPEDVETNCEWSAFSCF---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 vnvisdlkk-iedligsmhidatlytesdvhpsckvtamkcfllelqvislesgdasihd
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)B; AAX29479.
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                                                                                                                                                                                                                                           specific for epithelium-derived T-cell growth factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 AA;
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93US-0031399.
94US-0233606.
96US-0725969.
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25.9%;
                                                                                                                                                                              English.
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Pred. No. 0
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RESULT 15
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       their precursors) or radionuclides. ETF induces proliferation and/or differentiation of T cells (or their precursors), e.g. for use in establishing long term in vitro cultures; and is also used to treat gastrointestinal disease (e.g. enteritis or mucositis induced by chemotherapy or radiation, peptide ulcer, gastroenteritis, colitis, villus atrophy, malignancy and inflammatory bowel disease), to treat human immune deficiency virus infection or associated disease, or generally in any situation requiring stimulation of T or B cell proliferation, secretion of immunoglobulins or certain cytokines, increased anti-infectious disease immunity, induction of T-cell lytic activity or increased destruction of tumour or virus-infected cells. The present sequence represents the mature active sequence of simian ETF
                                                                                                                                                                                                                                                                                                                                                                 chemotherapy; radiotherapy; gut toxicity; cancer; side effect; tolerated dose.
          Claim 1; Fig 1; 33pp; English.
                                                    Stimulation of T-cells
                                                                                                                          Rauch
                                                                                                                                                                                                            22-FEB-1995;
04-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                         gastrointestinal disease;
                                                                                                                                                                                                                                                                                                                                                                                                                         CD8+;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mature simian epithelium-derived T-cell factor (ETF).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-2000
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                                                                                                                                                     (IMMV ) IMMUNEX CORP
                                                                                                                                                                                                 08-MAR-1993;
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                                                                                                                                                                                                                                                                                                            US5985262-A
                                                                                                                                                                                                                                                                                                                                        Mammalia.
                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                       epithelium-derived T-cell factor; T-cell; T-lymphocyte; iferation; differentiation; growth factor; precursor; matiferation; districtstinal, epithelium; cell culture; treatment; gastrointestinal disease; gastroenteritis; colitis;
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bB; AAZ38244.
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96US-0726817
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                                                                                                                                                                                               93US-0031399
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                                                                                                                           Eisenman
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                                                      human
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                                                                                                                           JR,
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Pred. No. 0.0031;
3; Mismatches 4
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                                                      immunodeficiency
                                                                                                                           Grabstein
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                                                                                                                           Anderson
                                                      virus
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CC This sequence represents mature simian epithelium-derived T-cell factor CC (ETF). This is a previously unidentified T-cell growth factor which CC stimulates precursor or mature CD4+ and CD8+ T-lymphocytes to proliferate CC and differentiate. It also promotes proliferation of the gastrointestinal CC epithelium. The protein can be used to promote long-term in vitro culture of T-lymphocytes and T-cell lines. ETF can be used for treating HIV CC infection, HIV-associated diseases, and other diseases or conditions CC where stimulation of T-cell proliferation would be desirable e.g., it CC ould be used to augment the destruction of tumour cells or virally-CC infected cells. ETF may also be used to treat or prevent gastrointestinal CC disease, including chemotherapy and radiotherapy associated enteritis, CC gastroenteritis, colitis, inflammatory bowel disease and villus atrophic CC disorders. Chemotherapy and radiotherapy associated enteritis (gut CC toxicity) results in bleeding and sepsis due to gastrointestinal flora centering the blood, and thus can limit the dosage of therapeutic agent administered to a cancer patient. ETF may therefore be used to increase CC the tolerated doses radiotherapy and chemotherapy.

38888888888888888888

Sequence 114 AA;

Qy В рЬ γQ Query Match 11.7%; Score 99.5; DB 21; Best Local Similarity 25.9%; Pred. No. 0.0031; Matches 30; Conservative 23; Mismatches 48; 43 IDIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF-----QKAQLKSANTGNNE 93 Length 114; Indels 15; Gaps 5.

Search completed: June 28, 2002, 07:46:29 Job time: $344\ \sec$

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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4: sp_human:*
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Gapop 10.0 , Gapext 0.5
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61 LPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHRL 120	1 MKSSEGNMERIVICLMYVIFLGTLYHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLYPEF 60 1 MKSSEGNMERIVICLMYIFLGTLYHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLYPEF 60		Query Match 100.0%; Score 850; DB 4; Length 162; Best Local Similarity 100.0%; Pred. No. 1.1e-79; Matches 162; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 162 AA; 18652 MW; 54EFD4EED3AB97FE CRC64;	8.1;	Nature 408:57-63(2000).	regulation of lymphocyte function.";	Maurer M., Kaushansky K., Holly R.D., Foster D.; "Interleukin 21 and its receptor are involved in NK cell expansion and	Rayond F., Ching A., Yao L., Smith D., Webster P., Whitmore T.,	Mudri S., Clegg C., Moore M., Grant F.J., Lofton-Day C., Gilbert T.,	Conklin D., Presnell S.R., Berry J., Shiota F., Bort S., Hambly K.,	Burkhead S., Heipel M., Brandt C., Kuijper J.L., Kramer J.,	Gross J.A., Johnston J., Madden K., Xu W., West J., Schrader S.,	Parrish-Novak J., Dillon S.R., Nelson A., Hammond A., Sprecher C.,	MEDLINE=20531754; PubMed=11081504;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).		21	(TrEMBLrel. 19, Last	(TrEMBLrel. 16,	01-MAR-2001 (TrEMBLrel. 16, Created)	Q9HBE4;	Q9HBE4 PRELIMINARY; PRT; 162 AA.	Q9нве4	RESULT 1

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MEDLINE=94200956; PubMed=8150599;
Gough K.H., Shukla D.D.;
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EMBL; D13695; BAA12854.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=31742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Johnsongrass mosaic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR004075; Intrlkn1_receptorI.
InterPro; IPR002052; N6_Mtase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR003598; Ig_c2.
InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                          ntervirology 36:181-192(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 LSSRTHGSE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DRLK-----FLPARVE----
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                                                                                                                                                                                                                                                                                                                                                                                                            nucleotide sequence
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IPR001410;
IPR001650;
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18
567 /
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                                                                                                                                                                                                                                                        (OCT-1993)
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64801 MW;
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DEAD.
Helicase_C
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Last
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                                                                                                                                                                                                                                                           EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9228CE227D95B0BC CRC64;
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                                                                                                                                                         databases
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Indels Length

37;

Gaps

7;

151

InterPro; InterPro;

IPR001730; IPR001456;

Peptidase_C4 Peptidase_C6

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RESULT
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Best Local s
Matches 25
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Pfam; PF00270; helicase_C; 1.
Pfam; PF00271; helicase_C4; 1.
Pfam; PF00863; Peptidase_C6; 1.
Pfam; PF00851; Peptidase_C6; 1.
Pfam; PF00167; Poty_Coat; 1.
Pfam; PF00177; Poty_Coat; 1.
Pfam; PF01577; Poty_P1; 1.
Pfam; PF00680; RNA_dep_RNA_pol; 1.
PF1NTS; PR00966; NIAPOTYPTASE.
                                          Matches
                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATP-binding; Helicase.
CHAIN 23 69
CHAIN 700 1046
CHAIN 1047 1098
CHAIN 1047 1757
CHAIN 1758 1803
CHAIN 1758 1803
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
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SEQUENCE
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                                                                                                                                                                                         "Organization and diversification of plasmid conclotide sequence of the CoIIb-P9 genome."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJEMBL; AB021078; BAA75140.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Shigella sonnei.
Plasmid Collb-P9
                                                                                                                                                                                                                                                                                  Sampei G., Mizobuchi K.;
                                                                                                                                                                                                                                                                                                        STRAIN-P9;
                                                                                                                                                                                                                                                                                                                                                                                          Shigella
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                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=624;
                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002540;
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                                                                                                                                                                           Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RKPPSTNAGRRQKHRLTCPSC-DSYEKKPPKEFLERFKSLLQKMIHQH 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVNALDQYEED-VKQICHYSEDAEARAFWKGFTENHTAQRREAHDHTNHEPV-MSVEECG 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLK 104
SSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAF - - - SCFQKAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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2234
2750
3052
                                                                                                                                                    899 AA;
                                            Conservative
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2749
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                                                             9.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                               gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                            22;
                                       Score 83; DB
Pred. No. 5.8;
22; Mismatches
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Last annotation update)
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Pred. No. 21;
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PROTEASE3.
6K1.
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LARGE NUCLEAR INCLUSION/POLYMERASE.
COAT PROTEIN.
4M; 08CD8831A73EBCA9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                    E7DB0164C54914E3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                 subdivision;
                                                          5.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae;
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                                            55;
                                                                                                                                                                                                                   databases
                                                                               Length 899
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                                            Indels
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                                          Gaps
    83
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RESULT
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Komano T., Nar
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and characterization of thin pili of IncIl
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MEDLINE-20196006; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
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Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
                                                                                                                                                                                                                                                                                                          Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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"Concerted action of three distinct domains in the DNA cleaving-
joining reaction catalyzed by relaxase (Tral) of conjugative pla
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RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Tbeywam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levisky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzpy D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Siden-Kiamos I., Simpson M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Yeb R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A.,
RA Zheng X.H., Zhong F.N., Rorley K.C., Wu D., Yang S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
BMBL, Ae003492; AAF48250.1; -
BMBL, Ae003492; AAF48250.1; -
BCQUENCE 566 AA; 60820 MW; 31FA41FA4ABF427F CRC64;
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Matches 24
                                                                          Query Match
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Q966R0;
O1-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
CALCIUM BINDING PROTEIN (
                                                                                                                                                        Nishio K., Yokoyama M., Maeda M.;
"Novel calcium binding proteins in Dictyostell
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ
EMBL; AB070450; BAB63908.1; -.
                                                                                                                                                                                                                                                                Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyosteliida; NCBI_TaxID=44689;
                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                      STRAIN=KAX4;
                                                                                                                                                                                                                                     SEQUENCE
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LNEIKPTILKCDKNKDRQ-----YSIDEIVQLLKKNSKNPERLAVLLFKSLNKKLDESIC
                            VNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNA 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCKTERGKPVQQLIDQFQAMIVQQQQQQQLSN
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                                                                                                                                          163 AA;
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rEMBLrel. 19, L
rEMBLrel. 19, L
3 PROTEIN CBP9.
                                                                                                                                            18924 MW;
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Pred. No. 4.8;
21; Mismatches
                                                            Score 81; DB
Pred. No. 1.3;
17; Mismatches
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GRRQKHRLTCPSCDSYEKKPP---KEFLERFKSLLQKMIHQH 151 FNDIDDREISKNCDKFQDKPEIDIESFLLRFDKNNDKMISHH 105

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RESULT
Q9VJL7
ID Q2
AC Q2
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DT 0:
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards G., Change M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Chanpe M., Pfeiffer B.D.,
RA Haller R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Gerry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cavley S., Dahlke C., Davenport L.B., Durkov B.C., Dunn P.,
RA Gerry J.M., Cavley S., Dahlke C., Ferraca C., Ferriera S., Fleisschmann W.,
RA Durbin K.J., Evangelista C.C., Ferraca C., Ferriera S., Fleisschmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.I., Harvey D., Haiman T.I., Hernandez J.R., Hunck J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Alalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalaii M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liaxo P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liaxo, Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Mcrkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.H.,
Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo K., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z. V. Wassarman D. A. Wainstock G. M. Weissenboth I.
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Q9VJL7;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotation update)
BG:DS02740.8 PROTEIN.
BG:DS02740.8 PROTEIN.
BG:DS02740.8 OR CG17328.
Grosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh. R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Glbbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;
PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6. PROSITE; PS50157; ZINC_FINGER_C2H2_2; 6. DNA-binding; Metal-binding; Zinc-finger_SEQUENCE 385 AA; 43943 MW; 24D0EAE4C
                                                                                                                                                                             InterPro; IPR000822; Znf-C2H
Pfam; PF00096; zf-C2H2; 6.
SMART; SM00355; ZnF_C2H2; 6.
                                                                                                                                                                                                                                                                                                                                                               EMBL; AE003650; AAF53516.1; -. HSSP; P08046; 1A11.
                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0028895; BG:DS02740.8.
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    24D0EAE4C5FD5DA6 CRC64;
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RESULT
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       Matches
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Q9NK60;
01-OCT-2000 (TrEMBLrel. 15, C
01-OCT-2000 (TrEMBLrel. 15, I
01-DEC-2001 (TrEMBLrel. 19, I
BG:DS02740.8 PROTEIN.
                                                                                                                                                                                                                                                                                          STRAIN-Y, CN BW SP;
Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G.,
Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle C.M.,
Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A.,
Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B.,
Tomorfan M.A., Mazda P., Moshrefi A.R., Moshrefi M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
MCBI_TaxID=7227;
                                                                                                                                                                                Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi M., Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A., Sethi H., Snir B., Svirskas R.R., Wan K.H., Weinburg T., Zhang R., Zieran L.L., Rubin G.M.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AB003415; AAF44998.1; -. HSSP; P08046; 1A1I.
Pfam; PF00096; zf-C2H2; 6.

SMART; SM00355; ZnF_C2H2; 6.

PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.

PROSITE; PS00028; ZINC_FINGER_C2H2_1; 6.

PROSITE; PS00157; ZINC_FINGER_C2H2_2; 6.

DNA-binding; Metal-binding; Zinc-finger.

DNA-binding; Metal-binding; Zinc-finger.

SEQUENCE 414 AA; 47307 MW; 182657C92E2E2D1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celniker S., Rubin G.M.; "An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moshrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K
                                                                                                                              InterPro; IPR000345; CytC_heme_bind
InterPro; IPR000822; Znf-C2H2.
                                                                                                                                                                     FlyBase; FBgn0028895; BG:DS02740.
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-99403001;
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Query Match Best Local

Similarity 37; Conserv

Conservative

22;

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Score 81; DB Pred. No. 3.8; 22; Mismatches

3.8 3.8

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64;

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A Choi K.D., Lillehoj H.S., Burnside J.;

A Choi K.D., Lillehoj H.S., Burnside J.;

A Choi K.D., Lillehoj H.S., Burnside J.;

A Choi K.D., Lillehoj H.S., Burnside J.;

A Choi K.D., Lillehoj H.S., Burnside J.;

B "Gallus gallus mRNA for II-15 EMBL/GenBank/DDBJ danger Submitted (MAR-1999) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Submitted (MAR-1995) to the EMBL/GenBank/DDBJ danger Subm
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Best Local S
Matches 34
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01-NOV-1999
01-NOV-1999
01-JUN-2001
                                                                                                                                                 O91Y09; PRELIMINARY; PRT; 1006 AA.
091Y09; 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Galliformes; Phasianidae; Phasiani
                PROTOCADHERIN ALPHA C2.
Mus musculus (Mouse).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Rod
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Burnside J., Sofer L.;
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01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
INTERLEUKIN-15 PRECURSOR (INTERLEUKIN 15 PRECURSOR).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTIFFLCAYVPKTEANHCKWSDVLKDLELIKTSEDIDVSLYTAN-----TYEDI 100
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        Chordata;
Rodentia;
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Pred. No. 2
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            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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C STRAIN-C57BL/6; TISSUE-Liven,
C STRAIN-C57BL/6; TISSUE-Liven,
C STRAIN-C57BL/6; TISSUE-Liven,
C STRAIN-C57BL/6; TISSUE-Liven,
C STRAIN-C57BL/6; TISSUE-Liven,
C STRAIN-C57BL/6; TISSUE-Liven,
C MEDLINE-C12125; PubMed-11318609;
AN Transcripts of Flizl, muller A.M.;
C "Transcripts of Flizl, a nuclear zinc finger protein, are
RT discrete foci of the murine fetal liver.";
RL Genomics 73:194-202(2001).
DR EMBL; AF061961; AF74513.1; -.
DR EMBL; AF061961; AF74513.1; -.
DR MGD; MGI:1930128; Flizl.
DR InterPro; IPR000771; 2f-CCCH.
DR Ffam; PF000642; zf-CCCH; 3.
DR SMART; SM00356; ZnF-C3H1; 3.
DR SMART; SM00356; ZnF-C3H1; 3.
DR SMART; SM00356; ZnF-C3H1; 3.
DR SMART; SM00356; ZnF-C3H1; 3.
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EMBL; AY013769; AAKZ8058.L; ...
SEQUENCE 1006 AA; 109491 MW; EB7E291
                                                                                                                                                                                                                                                                                                                        Q9JJ48
Q9JJ48;
Q1-OCT-2000
01-OCT-2000
01-DEC-2001
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Wu Q., Maniatls T.;
"A striking organization of
like cell adhesion genes.";
Cell 97:779-790(1999).
                                                                                                                                                                                     SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE=LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Large exons encoding multiple ectodomains are a feature of protocadherin genes."; Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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MEDLINE=20202599;
                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                 Eukaryota;
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                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
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%; Pred. No. 15;
14; Mismatches
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)., Myers R.M., Maniatis T
of mouse and home-
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01-MAY-2000
01-MAY-2000
01-JUN-2001
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"NEDO human cDNA sequencing project.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AKO58131; BAB71677.1; -. 682FB4EF7C6CC936 CRC64;
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25402 FIS, CLONE TST02870.
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                                                                                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda: Tracheata: Hexapoda: Insecta:
Pterygota: Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
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Last annotation update)
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RA Adams M.D., Celniker S.E., Hölt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Hölt R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Richards S., Asbburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chem L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chem L.X.,
RA Barladon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Ffeiffer B.D.,
RA Ballew R.M., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Mann. J.F., Apjayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Borkova D., Botchan M.R., Bouck J., Bayraktarogiu L., Beasley E.M.,
Ra Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Boshakov S.R.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chadra I.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chadra I.,
RA Gebris R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferrica S., Fleischmann W.,
RA Godek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Noshrefi A.,
RA Merkulov G., Schoel R., Nan E.,
RA Merkulov G., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Shue B. C., Siden Kiamos I., Si
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Best Local Similarity
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InterPro; IPR000734; Lipase.
Pfam; PF00151; lipase; 1.
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115 QPGFGEDEVTIVLTGLPKTSPAQQKAMRRLIQAYVQKYNL 154
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                                                                                GAKVIEKIYHVGQIK---HDLTPSFVPSPSNVPV---WIIKSNGQKVECKLNNYVETAKA 114
                                        NTGNNERIINVSIKKL-KRKPPSTNAGRR-----QKHRL 120
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Search completed: Job time: 230 sec June 28, 2002, 07:44:35

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Result
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Copyright (c) 1993 - 2000 Compugen Ltd
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ALIGNMENTS

interleukin-15 precursor -

RESULT 2 S29498 Lymphocyte antigen Ly84 precursor - mouse N;Alternate names: 38.5K T1 glycoprotein; ST2L protein C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 01-Dec-2000 C;Accession: S29498; A3541; S17657; S07054 R;Yanagdisawa, K.; Takagi, T.; Tsukamoto, T.; Tetsuka, T.; Tominaga, S. FEBS Lett. 318, 83-87, 1993 A;Title: Presence of a novel primary response gene ST2L, encoding a product highly si A;Reference number: S29498; MUID:93170492 A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-567 <yan> A;Cross-references: EMBL:D13695; NID:9286100; PIDN:BAA02854.1; PID:9286101</yan>	Qy 43 IDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNE 93 :::: : : : : : : : : : :	A; Restudes: 1-102 SGRAP A; Ross references: GB:U03099; NID:g493521; PIDN:AAA18416.1; PID:g493522 A; Note: the complete translation is not shown C; Superfamily: interleukin-15 C; Reywords: growth factor F; 49-162/Product: interleukin-15 #status predicted <mat> F; 83-133,90-136/Disulfide bonds: #status predicted F; 83-133,90-136/Disulfide bonds: #status predicted Query Match Best Local Similarity 25.9%; Pred. No. 0.18; Matches 30; Conservative 23; Mismatches 48; Indels 15; Gaps 5;</mat>	interleukin-15 precursor - green monkey C;Species: Cercopithecus aethiops (green monkey, grivet) C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 C;Accession: A53484 R;Grabstein, K.H.; Eisenman, J.; Shanebeck, K.; Rauch, C.; Srinivasan, S.; Fung, V.; Giri, J.G. Science 264, 965-968, 1994 A;Title: Cloning of a T cell growth factor that interacts with the beta chain of the A;Heteronce number: A53484; MUID:94233380 A;Accession: A53484 A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Bolecule type: mRNA

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R;Fominaga, S.I.

R;Fominaga, S.I.

R;Fominaga, S.I.

A;Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly si A;Title: A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly si cession: S07054; MUID:90092495

ccession: S07054

A;Residues: 1-328 (*SKECPSHIA' <TO2>
A;Cross-references: EMBL:Y07519; NID:g55517; PIDN:CAA68812.1; PID:g55518

A;Rote: It is uncertain whether Met-1, Met-7 or Met-19 is the initiator

C;GenetLos:

A;Gene: ST2

A;Map position: 1

A;Introns: 37/1; 97/2; 155/3; 210/1; 233/1; 280/2

C;Superfamily: interleukin-1 receptor type I

C;Keywords: 91ycoprotein

F;1-50/Domain: signal sequence #status predicted <SIG>
F;27-337/Product: ST2 protein #status predicted <MAT>

F;60,101,107,146,176,194,225,259,278/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                nikB protein - Escherichia coli plasmid
C:Speckes: Escherichia coli
C:Date: 12-Jul-1991 #sequence_revision
C:Accession: B38529
R:Furuya, N.; Nisioka, T.; Komano, T.
J. Bacteriol. 173, 2231-2237, 1991
                                               A:Title: Nucleotide sequence and functions A:Reference number: A38529; MUID:91177811 A:Accession: B38529 A:Status: preliminary A:Molecule type: DNA A:Residues: 1-899 <FUR>
A:Cross references: GB:D90273; NID:g217081:C:Genetics:
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A;Molecule type: DNA
A;Residues: 1-191,'V', 193-328,'SKECPSHIA'
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A; Cross-references: GB:M2843; NID:9201103; PIDN:AAA40160.1; PID:9201104
R; Tominaga, S.I.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Tetsuka,
Biochim. Biophys. Acta 1090, 1-8, 1991
B; Tittle: Molecular cloning of the murine ST2 gene. Characterization and A; Reference number: S17657; MUID:91355215
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A;Accession: A33541
A;Molecule type: mRNA
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A; Genome: plasmid
C; Superfamily: Es
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nenz, R.; Hoffmann, S.; Werenskiold, Natl. Acad. Sci. U.S.A. 86, 5708-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 PPSCNIPDYLMYSTVRGSDKNFKITCPTIDLYNWTAPVQWFKNCKALQEPRFRAHRSYLF 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDNVTHDDE 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LSSRTHGSE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPSTN-----AGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIHQH-----
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     Escherichia
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  coli
                                                                          NID:g217081;
nikB protein
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Pred. No. 1
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                                                                            PIDN:BAA14318.1;
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A;Cross-references: GB:M21442; NID:g213930; PIDN:AAA49637.1; PID:g213931 R;Schorpp, M.; Doebbeling, U.; Wagner, U.; Ryffel, G.U. J. Mol. Biol. 199, 83-93, 1988 A;Title: 5'-flanking and 5'-proximal exon regions of the two Xenopus alba;Reference number: S02692; MUID:88172470 A;Accession: S02693
                                                                                                                                        F;30/Binding site: copper (His) **status predicted F;80-88,101-117,116-127,147-192,191-200,223-269,268-276,288-302,301-312,339-384,383-3 F;256/Binding site: carbohydrate (Asn) (covalent) **status predicted
                                                                                                                                                                                                                                                                                                                    C;Keywords: carrier protein; duplication; glycoprotein; met F;1-18/Domain: signal sequence #status predicted <SIG>F;19-24/Domain: propeptide #status predicted <PRO>F;25-607/Product: 74K serum albumin #status predicted <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA, A; Residues: 459-502, T., 504-557 < WOL> A; Residues: 459-502, T., 504-557 < WOL> A; Cross-references: GB: M28276 A; Note: the authors translated the codon TAT for residue 63 as Thr A; Note: the authors translated in the liver as preproalbumin. It binds coppe C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds coppe C; Comment: Serum albumin is synthesized in the liver as preproalbumin. It binds coppe C; Comment: Serum albumin is synthesized in the liver as preproalbumin.
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R;Wolffe, A.P.; Glover, J.F.; Martin, S.C.; Tenniswood, M.P.R.; Williams, Eur. J. Biochem. 146, 489-496, 1985
A;Title: Deinduction of transcription of Xenopus 74-kDa albumin genes and A;Reference number: A05288; MUID:85126974
A;Accession: A05288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              e during development.
A;Reference number: A41682; MUID:89313788
A;Accession: B41682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              В
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                                                                                                                                                                                                                             F;220-393/Domain: serum albumin repeat homology <SA2>F;412-591/Domain: serum albumin repeat homology <SA3>
                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: serum albumin; serum albumin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Genetics:
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A; Residues: 1-48 <SCH>
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A; Residues: 3-607 < MOS>
                                                                                                                                                                                                                                                                                         F;32-201/Domain: serum albumin repeat homology <SAl>
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24.2%;
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                           Score 82;
Pred. No.
      Mismatches
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Gaps
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44 DIVDQLKNYVNDLVPEF - -

-LPAPEDVETNCEWSAFSCF----QKAQLKSAN 88

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A;Gene: FlyBase:Yp3
A;Gross-references: FlyBase:FBgn0004047
A;Gross-references: FlyBase:FBgn0004047
C;Superfamily: insect vitellogenin
C;Keywords: egg yolk; glycoprotein; phosphoprotein; sulfoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-420 < YAN>
A; Residues: 1-420 < YAN>
A; Cross-references: GB: X04754; NID: g8844; PIDN: CAA28451.1; PID: g8845
A; Cross-references: GB: X04754; NID: g8844; PIDN: CAA28451.1; PID: g8845
A; Garabedian, M.J.; Shirras, A.D.; Bownes, M.; Wensink, P.C.
Gene 55, 1-8, 1987
Gene 55, 1-8, 1987
A; Title: The nucleotide sequence of the gene coding for Drosophila me A; Reference number: A27388; MUID: 87305580
                                                                                                                                                                                                                                                                                                                                               itellogenin III precursor - fruit fly (Drosophila melanogaster)
Alternate names: yolk polypeptide ypIII; yolk protein 3
/Species: Drosophila melanogaster
C;Date: 04-Mar-1988 #sequence_revision 12-May-1994 #text_change 20-Aug-1999
C;Accession: A25876; A27388
R;Yan, Y.L.; Kunert, C.J.; Postlethwait, J.H.
Nucleic Acids Res. 15, 67-85, 1987
A;Title: Sequence hombologies among the three yolk polypeptide (Yp) genes in A;Reference number: A25876; MUID:87146365
A;Accession: A25876
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A25876
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S49882
                                                                                                                      A;Cross-references: GB:M15898; NID:g158815; PIDN:AAA29024.1; PID:g158816
                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-420 <GAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: GB:Z47047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-206 <HAM>
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A; Accession: S49882
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Best Local S
Matches 25
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                                                                                                            Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QATSVVNGLLSNLLPGVPKIRANNGKTSVNNGSKAQLIDRNLKKRVQLQNRDVHKIKKKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CEEEDKE - - KCFSEKMKQLMK - - - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RDHEHTSIKPEPEETCKLLKEHPDDLLSAFIHEEARNHPDLYPPAVLALTKQYHKLAEHC 191
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29; Conser
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1 protein Y18277.02c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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A;Cross-references: EMBL:x85807; NID:g1045249; PIDN:CAA59808.1; PID:g1045256 R;Van Dyck, L.; Skala, J.; de Wergifosse, P.; Purnelle, B.; Talla, E.; Nawrocki, submitted to the Protein Sequence Database, May 1996 A;Reference number: S64428 A;Reference number: S64428 A;Recession: S64459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Saccharomyces cerevisiae C;Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #text_change 29-Oct-1999 C;Accession: S60441; S64459 R;Skala, J; Nawrocki, A; Goffeau, A. Yeast 11, 1421-1427, 1995
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S60441
 ureidoglycolate N; Alternate name
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A; Map posi:
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A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-864 < VAN>
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A; Residues: 1-864 < SKA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein YGR150c - yeast (Saccharomyces cerevisiae) N;
Alternate names: hypothetical protein \mathsf{G6642}
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Best Local Similarity
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                                                                                                             AKNLFDRSHSN 161
                                                                                                                                                --HLSSRTHGS 159
                                                                                                                                                                                                                         HRLTCPSCDSYEKKPPK--
                                                                                                                                                                                                                                                                                             PEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQK 117
                                                                                                                                                                                                                                                                                                                                                                        RSSPGNMERIVIC----LMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLV 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAKVIEKIYHVGQIK---HDLTPSFVPSPSNVPV---WIIKSNGQKVECKLNNYVETAKA 114
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                                                                                                                                                                                     NSIAPISEDSRNVNVTKTSSVPNEEKSKNLSDLIHSSFLEKMDHLVPKVIRERVADDDIL 150
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                 hydrolase
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protein
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22.5%;
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 (EC 3.5.3.19) -
YIR032c
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Pred. No. 48;
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                   yeast (Saccharomyces cerevisiae)
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C:Species: Saccharomyces cerevisiae
C;Date: 31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change 21-Jul-2000
C;Accession: $42022; $48494
R;Yoo, H.S.; Cooper, T.G.
Yeast 7, 693-698, 1991
A;Title: The ureidoglycollate hydrolase (DAL3) gene in Saccharomyces cerevis A;Reference number: $42022; MUID:92133160
A;Accession: $42022
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A; Residues: 1-195 < YOO>
A; Cross references: EMBL:M64778; NID:g171369; PII
R; Rowley, K.
submitted to the EMBL Data Library, October 1994
A; Reference number: $484478
A; Accession: $48494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 19-May-2000
C;Accession: S42632
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842632
Fit-1S protein precursor - rat
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Keywords: allantoin degradation; hydrolase; lipoprotein; methylated carboxyl end; pren F;192/Binding site: farnesyl (Cys) (covalent) #status predicted F;192/Modified site: methyl ester carboxyl end (Cys) (in mature form) #status predicted
В
                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-336 <BER>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Bergers, G.; Reikerstorfer, A.; Braselmann, EMBO J. 13, 1176-1188, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-195 < ROW>
                                                                                                                                                                                                                                                                                                                                                                                                                                           Title: Alternative promoter usage of the Fos-responsive gene Fit-1 generates mRNA reference number: $42632; MUID:94178260 recession: $42632; Status: preliminary
                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local 9
                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: SGD:S0001471; MIPS:YIR032c ap position: 9R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: SGD:DAL3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cross-references: GB:Z47047; EMBL:Z38061; NID:g603997; PID:g763377; MIPS:YIR032c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genetics:
                                                                                    103
  156 NCKALQGPRFRAHMS
                                         139 RFKSLLQKMIHQHLS 153
                                                                                                                           89
                                                                                                                                                                    49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           \mathfrak{u}
                                                                                                                                                                                                             43 IDIVDQLKNYVNDLVP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 VHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQ 83
                                                                                  TGS----LNVTIYK---RPPNCKIPDYMMYSTVDGSDKNSKITCPTIALYNWTAPVQWFK 155
                                                                                                                                                                    INPVEWYYSNTNERIPTOKRNRIFVSRDRLKFLPAKVE-----DSGIYTCVIRSP-ESIK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LKSANTGNNERIINVSIKKLKRKPPST 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEKGANQGT---AIKLLQ----VSQVENKSTSKVP---
                                                                                                                           TGNNERI INVSIKKLKRKPP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNRVFTQGSNQAISHSIKVLEKHPCST 99
                                                                                                                                                                                                                                                         30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 27.6
24; Conservative
                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                          8.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8.9%;
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                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                          -----EFLPAPEDVETNCEWSAFSCFQKAQLKSAN 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NID:g171369; PIDN:AAA73025.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 76;
Pred. No.
                                                                                                                                                                                                                                                                            Score 75.5;
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                       Mismatches
                                                                                                                         -STNAGRROKHRLTCPSCDSYEKKPPKEFLE 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DВ
11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.; Graninger, P.; Busslinger,
                                                                                                                                                                                                                                                                                                DB
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                                                                                                                                                                                                                                                       42;
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                                                                                                                                                                                                                                                                                           Length 336;
                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomyces cerevisiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NWNLFRCFPQPH 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PID:g171370
                                                                                                                                                                                                                                                       37;
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RESULT 11
S24407
                                  QΥ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Davidson, S.; Wohldmann, P. submitted to the EMBL Data Library, July 1996 A;Description: The sequence of C. elegans cost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein F45F2.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C;Accession: T28957
 밁
                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-1206 <JAC>
A;Cross-references: EMBL:X62379; NID:g51552; PIDN:CAA44244.1; PID:g51553
                                                                                                                                                                                                                                                                                               A; Reference number: S24407;
A; Accession: S24407
                                                                                                                                                                                                                                                                                                                A; Title: A variant limb deformity transcript A; Reference number: S24407; MUID:92112033
                                                                                                                                                                                                                                                                                                                                                  R; Jackson-Grusby, L.; Kuo, A.; Leder, Genes Dev. 6, 29-37, 1992
                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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A; Introns: 1/2;
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A; Residues: 1-406 < DAV>
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A; Accession: T28957
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                                                                                                                                                                                                                                                                                                                                                                                                                                             formin isoform IV -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: CESP:F45F2.11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references:
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                                                                                                                                            Query Match
Best Local S
Matches 37
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 1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             127 VSFNAFDEVKRAAQAKTAKSPSTSSLERRAQRF-CPA-DFQPLPPPHIYIEMIRTLAP--
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DYVVKYYLRYYDQEAGTDKSVFPLPEPQDFFLASQVKFEDLLK-DLRKLKRQLEAS----
                                  DLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGR 114
                                                                                                        RSSPG--NMERI--VICLMVIFLGTLVHKSSSQGQ-DRHMIRMRQLIDIVDQLKNYVN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IHQHL 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KSSPQSSDENFFKRLQWGKIRLELK-----TPEFLKESSELEIEKNEKSGIQKCGENEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLP----
                                                                        RASKGLLHMKSVKDILALILAFGNYMNGGNRTRGQADGYSLEILPKLKDVKSRDNGMNLV 1012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -HQYI 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IINVSIKKLKR-----KPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKM 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENEEKCEFRPVVTPNEIDSHKEWYHRLLMLKLEYKRGERGAFPPFPPPPPPSMMIAASNA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----SAFSCFQKAQLKSANTGNNER
                                                                                                                                              l Similarity
37; Conserv
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38; Conserv
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24/2; 143/3; 307/2; 338/2
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                                                                                                                                                Conservative
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ce: strain Bristol N2; clone F45F2
                                                                                                                                                                                                                                                                                                                                                                                                                                               mouse
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20.5%;
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22.0%;
                                                                                                                                                41; Mismatches
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Pred. No. 26;
                                                                                                                                                               Score 75.5;
Pred. No. 84;
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                                                                                                                                                69;
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                                                                                                                                                21;
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                                                                                                                                                Gaps
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hypothetical protein DKFZp434C0816.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 04-Feb-2000
 밁
                                 Qy
                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-286 <GLA>
A;Cross-references: GB:AE002149; GB:AF222894; NID:g6899503; PIDN:AAF30917.1; GSPDB:GN001
A;Experimental source: serovar 3; biovar 1
                                                                                                                                                                                                                                                                                                                                                                                                                    pothetical protein UU505 [imported] - Ureaplasma urealyticum
Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
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R;Koehrer, K.; Beyer, A.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, January 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дδ
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                                                                                                                                                                  A; Genetic code: SGC3
                                                                                                                                                                                   A; Gene:
                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                             A; Reference number: A82870
A; Accession: F82881
                                                                                                                                                                                                                                                                                                                                                                   R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, submitted to GenBank, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-321 <AAA>
Cross-references: EMBL:AL137283
Experimental source: adult testis; clone DKFZp434C0816
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: 223037
A; Accession: T46352
                                                                                                                                                                                                                                                                                             A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                  A; Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mi
                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 LHSEDTLOMDGHILDSKRYAVIGADLRDLSELEEKLKKCNMNTQLPTLLIAECVLVYMTP 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251 QKERLLSNGWETASAVDMMELYNRLPRAEVSRIESLEFLDEMELLEQLMRHYCLCWATKG 310
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GGIISLLIVITAIILGVILSTQNTNKISKKEPLTQIEDNINNKKQDAH--KVNENITIID 78
                                 GNMERIVICLMVIFLGTLVHKS------SSQGQDRHMIRMRQLIDIVD 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQSANLLKWAANS-FERAMFINYEQVNMG--DRFGQIMIENLRRRQCDLAGVETCKSLES 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EDVETNCEWSAFSCFQKAQL---KSANTGNNERIINVSIKKLKRKP-----PSTNAGRR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QKHRL-----TCPSCDSYE--KKPPK------EFLERFKSLLQKMIHQHLSSRTHG 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
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                                                                                         Similarity
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                                                                        Conservative
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23.0%;
                                                                    8.8%; Score 74.5; 1
20.6%; Pred. No. 22;
tive 38; Mismatches
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Pred. No.
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                                                                                                       DB 2;
                                                                      59;
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                                                                                                         Length 286;
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K;COLLIN, T.; Lory, P.; Taviaux, S.; Courtieu, C.; Guilbault, P.; Berta, P.; Nargeot, Eur. J. Biochem. 220, 257-262, 1994
A;Title: Cloning, chromosomal location and functional expression of the human voltage A;Reference number: $41211; MUID:94164167
A;Stratus. ~~~~1211
                                                                                                                                                                                            R:Favello, A.D.

Submitted to the EMBL Data Library, May 1993

A;Description: Sequence of the C. elegans cosmid C14B9

A;Reference number: S44617

A;Accession: S44759

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-789 <FRNY
                                                                                                                                                                                                                                                                                                                                                                          $44759
$C1489.5 protein - Caenorhabditis elegans
$C;Species: Caenorhabditis elegans
$C;Species: Caenorhabditis elegans
$C;Date: 14-Sep-1994 #sequence_revision 12-May-1995 #text_change 09-Sep-1997
$C;Accession: $44759
$R;Favello, A.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-482 <COL>
A;Cross-references: GB:L27584; NID:g443663; PIDN:AAA19799.1; PID:g443664
C;Superfamily: human voltage-dependent calcium channel beta chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         voltage-dependent calcium channel protein - human C;Species: Homo sapiens (man) C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 18-Aug-2000 C;Accession: S41211 R;Collin, T:: Lory, P:: Taviaux, S:: Courtieu, C:: Guilbault, P:: Berta, P.
                                                                                                                        A; Introns: 61/3; 129/2; 147/3; 191/3; 279/3; 368/3; 392/3; 627/3; 710/1; 731/1
                                                                                                                                                   C; Genetics:
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                                                                                                                                                                      A;Cross-references: EMBL:L15188; NID:g289640; PID:g289646
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Local Similarity 20.8%;
                        Local Similarity
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24.3%;
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                     Score 74.5;
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Pred. No. 39;
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18 IFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPA-PEDVETNCEWSAF 76

Job t	Searc	DЪ	Qγ	DЪ	Qγ	Db
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IR11_MOUSE
IL15_BOVIN
IL15_SHEEP
ALIA_YEAST
IDH_AZOVI
KNS5_HUMAN
IL15_PIG
INS5_HUMAN
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71 CEWSAFSCF	14 CLMVIFLGT : 30 CIPVFILSC	Match Local Simi mes 38;	EMBL; AF108148; InterPro; IPR00 Pfam; PF02372; Cytokine; Glyco SIONAL 1 PROPEP 3 90 CHAIN 49 DISULFID 90 CARBOHYD 104 CARBOHYD 107 CARBOHYD 162 SEQUENCE 162	tween tween e Europ e by dified tities send a	SEQUENCE FROM N.A. SEQUENCE FROM N.A. TISSUE-Lymph node; Barger A.B., Dean G.A., Lavoy, Submitted (NOV-1998) to the EM. -I- FUNCTION: CYTOKINE THAT ST LYMPHOCYTES. STIMULATION B WITH COMPONENTS OF IL-2R, GAMMA BUT NOT IL-2R ALPHA -I- SUBCELLULAR LOCATION: SecrI- SIMILARITY: BELONGS TO THE	D	30-MAY-2000 30-MAY-2000 30-MAY-2000 30-MAY-2000 Interleukin-	1 LCA 15_FELCA		69.5 69.5 69.5 69.5 69.5 69.5 69.5
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SAN	KSSSQGQD :: KTEANWQD	0 # ; 5 #	3.1; - Serleu Signa	tute tics fics titu ent ent ense	LAVOY TO THE EM TO THE THAT ST BULATION B TL-2R 2R ALPHA 2R ALPHA 1TON: Sect	ıs (Cat) Chordata Carnivor	(III)			
QKAQLKSANTGNNERIINVS	DRHMIRMR	Score Pred. 25; Mis	NA POR OCC.	y is copyright. I nstitute of Bioin rmatics Institute institutions as atement is not re license agreement license@isb-sib.c	Lavoy A.S.; the EMBL/GenBani FHAT STIMULATES: YITON BY IL-15 RI LT-2R, INCLUDING ALPHA (BY SIMIL N: Secreted. TO THE IL-15 FAL TO THE IL-15 FAL	; Crani a; Fiss	eated) st sequence st annotatio (IL-15).	PRT;	ALIG	YMP3_CAEEL SMC3_YEAST BUD3_YEAST Y413_RICPR Y564_TREPR Y564_TREPR Y61_MOUSE EMN1_MOUSE Y832_METJA IL4_CANFA ETSI_BUCAP PMS1_HUMAN NJB_HAEIR NJH2_SCHPO
NVSIKKLKRKPPSTNAGRRQKHRLT	SQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFL: : :	re 106.5; DB 1; d. No. 0.0042; Mismatches 58;	15. CNAC CNAC	roduce ics a ics are re are as its Usag http:/	LAVOY A.S.; the EMBL/GenBank/DDBJ databas 'HAT STIMULATES THE PROLIFERAT TION BY II-15 REQUIRES INTERA 'L-2R, INCLUDING IL-2R BETA AN ALPHA (BY SIMILARITY). 'I Secreted. TO THE IL-15 FAMILY.	ata; Vertebrata ipedia; Felidae	e update) ion update)	162 AA.	ALIGNMENTS	AST AST AST AST AST AST AST AST AST AST
	, 7	Length 162; Indels 25	.) (POTENTIAL) .) (POTENTIAL) :RC64;	through d the E no rest content by an www.isb-	BJ databases. PROLIFERATION OF T- RES INTERACTION OF I ZR BETA AND PROBABLY Y).	; Euteleostomi; ; Felis.				Q10947 P47037 P25558 Q9zdb9 Q9zdb9 Q958242 Q058242 Q77762 Q85297 P54277 P54277 P5424411 Q92347
CP 123	APEDVETN 70 SDVHPN 82	?; ?5; Gaps	AL).	collabor outstat tions on in no or comme	1L-15 BLY IL-2R	:omi;				caenorhabdi saccharomyc saccharomyc rickettsia treponema p mus musculu methanococc canis famil buchnera ap homo sapien haematobia schizosacch
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  밁
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 3).

Meazza R., Ferrini S.;

Meazza R., Ferrini S.;

"Expression of two IL-15 mRNA isoforms in humber of different contains and the contains are contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the contained to the con
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Srinivasan S., Fung V., Beers C., Richardson
Ahdieh M., Johnson L., Alderson M.R., Watson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P40933; Q93058; O43512; O00440; Q9UBA3; O1-FEB-1995 (Rel. 31, Created) O1-FEB-1995 (Rel. 31, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat. Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HUMAN
  -
                                                                                                                                      "IL15
                                                                                                                                                                                                                                                                                                                                                                                       "Generation of secretable and nonsecretable interl through alternate usage of signal peptides."; Proc. Natl. Acad. Sci. U.S.A. 94:14444-14449(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Testis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oncogene 12:2187-2192(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Orengo A.M., Colombo M.P., Azzarone B., Ferrini S.;
"Identification of a novel interleukin-15 (IL-15) transcript isoform
generated by alternative splicing in human small cell lung cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96218668; PubMed-8668345;
Meazza R., Verdiani S., Biassoni R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-1995) to
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                                                                                                                                                                                  TISSUE=Epidermis;
                                                                                                                                                                                                       SEQUENCE OF 49-162
                                                                                                                                                                                                                                                       Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bamford R.N., Waldmann T.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tagaya
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-98070771; PubMed=9405632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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              15 expression in human keratinocytes.";
mitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CYTOKINE THAT STIMULATES THE PROLITERATION OF T-
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-
GAMMA BUT NOT IL-2R ALPHA.
  SUBCELLULAR
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                                                                                                                                                       M.A., Jacques
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ξ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ng of a T cell growth factor that interacts with
interleukin-2 receptor.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (IL15-S21AA ISOFORM)
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(IL15-S48AA).
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B., Ferrini S.;
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n J., Son J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                     interleukin
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signal pepti
| databases.
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, Schoenborn M.A.,
anderson D.M.,
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  IL15-S21AA
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peptides.
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EMBL; U14407; AAA21551.1; -. EMBL; X91233; CAA62816.1; -. EMBL; X94223; CAA63914.1; -. EMBL; X94222; CAA63913.1; -. EMBL; AF031167; AAB97518.1; -. EMBL; Y09908; CAA71044.1; -. EMBL; Z38000; CAA86100.1; -. EMBL; Z38000; CAA86100.1; -.
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DISULFID
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                                                                                                CONFLICT
                                                                                                                                                                                                                                                                                            Cytokine;
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                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                            InterPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial infections as its content is the commercial in the statement is not removed. Usage by and for commercial interpretations are supplied to the commercial interpretations and the statement is not removed. Usage by and for commercial interpretations are supplied to the commercial interpretation of the statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS: 3 ISOFORMS; IL15-S48AA (SHOWN HERE), IL15-S21AA AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING. TISSUE SPECIFICITY: MOST ABUNDANT IN PLACENTA AND SKELETAL MUSC IT IS ALSO DETECTED IN THE HEART, LUNG, LIVER AND KIDNEY. IL15-S21AA IS PREFERENTIALLY EXPRESSED IN TISSUES SUCH AS TESTIS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE IL-15 FAMILY.

DATABASE: NAME=R&D Systems' cytokine source book: IL15;

WWW-"http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=209".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECRETED, BUT RATHER IS STORED INTERNUCLEUS AND CYTOPLASMIC COMPONENTS.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; I
IL15-S21AA AND 3; ARE PRODUCED BY A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THYMUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     s requires a license agreement (S an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                                            IPR003443;
                                                                               141
162 AA;
                                                                                                                                                                               30
49
83
83
90
127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BUT RATHER IS STORED INTRACELLULARLY,
                                                                                                                                                                                                                                                                                                             IL15;
                                                                               141
18086
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162
133
136
136
127
37
               11.7%;
25.9%;
                                                                                                                                                47
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                                                                                                                                                                                                                                                                              Signal; Alternative POTENTIAL.
                                                                                  WW;
Score 99.5; D
Pred. No. 0.01
23; Mismatches
                                                                                                            POTENTIAL.

N-LINKED (GLCNAC. . .) (POTENTIAL).

MRISKPHLESISIQCYLCLLLNSHFLTEAGIHVEIIG ->

MVLGTIDLCS (IN ISOFORM IL15-921AA).

MRISKPHLRSISIQCYLCLLLNSHFLTEAGIHVEILGCFSA

GLPKTE -> MDFQVQIFSFLLISASVIMSR (IN
                                                                               ISOFORM 3).
E -> K (IN REF. 4); 0CE0520C1D8379E2
                                                                                                                                                                                                                              INTERLEUKIN-15.
POTENTIAL.
                                                                                                                                                                                                                                                              POTENTIAL
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RESULT
IL15_CH
                                                                        IL15_CERAE
IL15_CERAE
P40221;
01-FEB-1995
01-FEB-1995
15-DEC-1998
                                                               01-FEB-1995 (Rel. 3
01-FEB-1995 (Rel. 3
15-DEC-1998 (Rel. 3
Interleukin-15 prec
Cercopithecinae; NCBI_TaxID=9534;
                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                               Eukaryota;
                                          Cercopithecus
                                          aethiops (Green
                                                              el. 31, Created)
el. 31, Last sequence up
el. 37, Last annotation
precursor (IL-15).
                                                                                                                    STANDARD;
           Cercopithecus
                              Chordata;
                     Craniata; Vo
Catarrhini;
                                          monkey)
                                                                                                                      PRT;
                                                                                    update)
                                                                                                                     162
                                            (Grivet).
                                                                         update)
                      Vertebrata; Eutele
i; Cercopithecidae;
                                                                                                                     ₿
                                 Euteleostomi;
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110

TVENLII -- LANNSLSSNGNVTES -- -GCKECEELEEKNIKEFLQSFVHIVQMFIN RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISLESGDASIHD

160

94 51 Matches Query Match Best Local

30;

Conservative

23;

48;

Indels

15;

Gaps

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-QKAQLKSANTGNNE

93

Similarity

43

IDIVDQLKNYVNDLVPEF----LPAPEDVETNCEWSAFSCF---

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                                                                                                                                                                                                                                                                    RESULT
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Best Local S
Matches 30
                                                                                                                                                                                      P48092;
01-FEB-1996
01-FEB-1996
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
CARBOHYD
        TISSUE=Blood;
MEDLINE=96003435; PubMed=7561102;
Villinger F.J., Brar S.S., Mayne A.E., Chikkala N.,
"Comparative sequence analysis of cytokine genes fro
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ahdieh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grabstein K.H., Eisenman J., Shan Srinivasan S., Fung V., Beers C.,
                                                                                                         Cercopithecinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- SUBCELLULAR LOCATION: Secreted.
-i- SIMILARITY: BELONGS TO THE IL-15 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                          NCBI_TaxID=9544;
                                                                                                                                              Macaca mulatta (Rhesus macaque).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF02372; IL15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Science 264:965-968(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=94233380; PubMed=8178155;
                                                                  SEQUENCE FROM
                                                                                                                                                                         Interleukin-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *Cloning of a T cell
                                                                                                                                                                                                                                         L15_MACMU
                                                                                                                                                                                                                                                                                                           110
                                                                                                                                                                                                                                                                                                                                                             51 VNVISDLKK-IEDLIQSMHIDATLYTESDVHPSCKVTAMKCFLLELQVISHESGDTDIHD
                                                                                                                                                                                                                                                                                                                                                                                      43 IDIVDQLKNYVNDLVPEF-----LPAPEDVETNCEWSAFSCF----QKAQLKSANTGNNE
                                                                                                                                                                                                                                                                                                                                  94 RIINVSIKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R GAMMA BUT NOT IL-2R ALPHA.
                                                                                                                                                                                                                                                                                                        TVENLII--LANNILSSNGNITES---GCKECEELEEKNIKEFLQSFVHIVQMFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U03099; AAA18416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ein K.H., Eisenman J., Shanebeck K., Rauch C.,
asan S., Fung V., Beers C., Richardson J., Schoenborn
M., Johnson L., Alderson M.R., Watson J.D., Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
primates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003443;
                                                                                                                                                                       6 (Rel. 33, Creats) (Rel. 33, Last) (Rel. 37, Last) (1-15 precursor)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
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49
83
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127
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                                                                 N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΑA;
                                                                                                                                                                                                                                         STANDARD;
                                                                                                         Macaca.
                                                                                                                                                                                    33, Created)
33, Last sequence up
37, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48
162
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136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth factor that interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin_15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                        (IL-15).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                  23;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 94.5; DB Pred. No. 0.054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -LINKED (GLCNAC. . .) (P
1BF9A82644E1C9B7 CRC64;
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                                                                                                                                                                                                                                         162
                                                                                                                                                                                    update)
                                                                                                                                  Vertebrata; Euteleostomi;
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                                                                                                                    Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 162;
               from
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                          Ansari A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL).
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRL1_MOUSE STANDARD; PRT; 337 AA. P14719; P14719; O1-APR-1990 (Rel. 14, Created) O1-APR-1990 (Rel. 14, Last sequence update) O1-MAR-2002 (Rel. 41, Last annotation update) Interleukin 1 receptor-like 1 precursor (ST2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                            "A putative protein of a growth specific cDNA from BALB/c-3T3 cells is highly similar to the extracellular portion of mouse interleukin receptor.";
                                                                                                                                                                                                           STRAIN=BALB/C;
MEDLINE=90092495;
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Lymphocyte antigen 84). ILIRL1 OR ST2 OR STE2 OR LY84.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ptam;
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                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                           Tominaga S.;
                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WITH COMPONENTS OF IL-2R, GAMMA BUT NOT IL-2R ALPHA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVENLII -- LANNILSSNGNITES -- -- GCKECEELEEKNIKEFLQSFVHIVQMFIN
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PF02372; IL15; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31
162
                                       258:301-304(1989)
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                                                                                                                                                                                                               PubMed=2532153;
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N-LINKED (GLCNAC.
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I -> T.
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Pred. No. 0.05
23; Mismatches
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Tominaga S.I., Jenkins N.A., Gilbert D.J.,

Copeland N.

MEDLINE=91355215; PubMed=1832015;

TISSUE-Spleen;

SEQUENCE FROM N.A.

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the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CELL CYCLE.
-1- SIMILARITY: CONTAINS 3 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS
-1- SIMILARITY: STRONG, TO INTERLEUKIN-1 RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -! - DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity to the gene encoding carcinoembryonic antigen."; Proc. Natl. Acad. Sci. U.S.A. 86:5708-5712(1989).
-i- FUNCTION: POSSIBLY INVOLVED IN REGULATION OF T-LYMPHOCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
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"Serum- and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of the murine ST2 gene.
chromosomal mapping.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin
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                                                                                                           DQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRK 106
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PPSCNIPDYLMYSTVRGSDKNFKITCPTIDLYNWTAPVQWFKNCKALQEPRFRAHRSYLF
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M24843; AAA40160.1;
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                                                                                                                                                       Conservative
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IGC2; 2.
domain; Glycoprotein; Repeat; Signal.
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SEQUENCE
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01-NOV-1997 (Rel. 3
15-DEC-1998 (Rel. 3
Interleukin-15 prec
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DISULFID
CARBOHYD
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"Cloning and expression of bovine interleukin-15: analysis and modulation of transcription by exogenous stimulation.";

J. Interferon Cytokine Res. 17:473-480(1997).

-i- FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15 WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).

-i- SUBCELLULAR LOCATION: Secreted.
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                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed
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01-NOV-1997
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Pfam; PF02372;
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                                                 111 IENLTMLANSNISSIENKTELGCKECEELEEKSIKEFLKSFVHIVQMFIN
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                                                                       IKKLKRKPPSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERFKSLLQKMIH
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P14872;
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01-NOV-1990
01-NOV-1995
74 kDa seru
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Q9XSJ6;
16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Circulating in efferent lymph.";

J. Interferon Cytokine Res. 0:0-0(1999).

FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATION OF T-
-IXMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERACTION OF IL-15
WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA AND PROBABLY IL-2R
GAMMA BUT NOT IL-2R ALPHA (BY SIMILARITY).
                                                           XENLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria; Ceta
Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Last sequence up 16-OCT-2001 (Rel. 40, Last annotation Interleukin-15 precursor (IL-15).
                                                                                                                                                                                                                                                                                                                                                       SIGNAI
                                                                                                                                                                                                                                                                                                                                                              Cytokine;
                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02372; IL15;
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          1-APR-1990
1-NOV-1990
1-NOV-1995
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                                                                                                  LGCKECEELEKKSIKEFLKSFVHIVQMFIN
                                                                                                                                                                                                   ICLM------VIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDL-VPE 59
                                                                                                                     LTCPSCDSYEKKPPKEFLERFKSLLQKMIH
                                                                                                                                         TLYTESDAHPNCKVTALQCFLLELRVILHESKNAAIYEI-IENLTMLADRNLSSIENKTE
                                                                                                                                                          FLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKPPSTNAGRRQKHR 119
                                                                                                                                                                                 LCLLLNSHFLTEAGIHVFILGCI----
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                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
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16, Last sequence up
32, Last annotation
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  precursor.
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EMBL; M28276; AAA49642.1; -. PIR; B41682; ABXL/72. HSSP; P02768; 1BJ5.
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PRINTS; PR00802; SERUMALBUMIN.
ProDom; PD002486; Serum_albumir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Williams J.L., Tata J.R.;
"Deinduction of transcription of Xenopus 74 kDa destabilization of mRNA by estrogen in vivo and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schorpp M., Doebbeling U., Wagner U., Ryffel G.U.; "5'-flanking and 5'-proximal exon regions of the two Xenopus albumin genes. Deletion analysis of constitutive promoter function."; J. Mol. Biol. 199:83-93(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolffe A.P., Glover J.F., Williams J.L., Tata J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Schoenberg D.R.; "xenopus laevis serum albumin: sequence of the complementary "xenopus laevis serum albumin sequence of the complementary decoxyribonucleic acids encoding the 68- and 74-kilodalton peptide and the regulation of albumin gene expression by thyroid hormone during development.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xen
NCBI_TaxID=8355;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                       SMART; SM00103; ALBUMIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85126974; PubMed=3971963;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF F
BINDING CAPACITY FOR WATER, CA++, NA+, K+, FAI
BILIRUBIN AND DUGGS. ITS MAIN FUNCTION IS THE
COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
SUBCELLULAR LOCATION: EXTRACELLULAR.
TISSUE SPECIFICITY: PLASMA.
DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
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European Bioinformatics Institute.
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                                                                                                                                                                                                                                                             Metal-binding;
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                                                                                                                                                                                                                                                                                                                                                                                     IPR000264; Serum_albumin.
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                                                                                                                                                                                                                                                            MEDLINE-97449311; PubMed-9305780;
Canals A., Grimm D.R., Gasbarre L.C., Lunney J.K., Zar Molecular cloning of cDNA encoding porcine interleuk in Gene 195:337-339(1997).

-I FUNCTION: CYTOKINE THAT STIMULATES THE PROLIFERATI LYMPHOCYTES. STIMULATION BY IL-15 REQUIRES INTERAC WITH COMPONENTS OF IL-2R, INCLUDING IL-2R BETA ANI GAMMA BUT NOT IL-2R ALFIA (BY SIMILARITY).

-! SUBCELLULAR LOCATION: Secreted.

-! SIMILARITY: BELONGS TO THE IL-15 FAMILY.
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01-NOV-1997
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                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                        InterPro;
                                                              EMBL; U58142; AAB72031.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig).
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                     Pro; IPR003443;
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Glycoprotein;
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(Rel. 35, Last sequence up)
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-15 precursor (IL-15).
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                                          Interleukin_15
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Pred. No. 3.5;
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592BA4177A36B66B CRC64;
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There are no restrictions
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interleukin-15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., F Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D. Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C / AB972;
Barrell B.G., Badcock K.,
Churcher C.M., Connor R.,
                                                                                                                                                                                                                                                                                                    SGD; S0001389; YIL127C.
Hypothetical protein.
SEQUENCE 206 AA; 238
                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Walsh S.V., Whitehead S.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Saccharomycetales;
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Eukaryota; Fungi; Ascomycota; Saccharomyc
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                                                                                                                                     QLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQLKSANTGNNERIINVSIKKLKRKP 107
                                           PSTNAGRRQKHRLTCPSCDSYEKKPPKEFLERF - - KSLLQKMIHQHLSSRT
                                                                                          QATSVVNGLLSNLLPGVPKIRANNGKTSVNNGSKAQLIDRNLKKRVQLQNRDVHKIKKKC
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kDa protein in MET18-STH1
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K., Fraser
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RESULT 1
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KNS5_HUMAN
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                                Q02241;
01-JUL-1993 (Rel. 2
16-OCT-2001 (Rel. 4
01-MAR-2002 (Rel. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Edwards D.J., Heinrikson R.L., Chung A.E.;
"Triphosphopyridine nucleotide specific isocitrate dehydrogenase Azotobacter vinelandii. Alkylation of a specific methionine resid and amino acid sequence of the peptide containing this residue.", Biochemistry 13:677-683(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDH_AZOVI
P16100;
                                                                                               KNS5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Sahara T., Suzuki M., Te Submitted (OCT-1995) to
                   Mitotic
                                                                                                                                                                                                                                                                                                                                                                                                        Oxidoreductase; NADP; Phosphorylation; Glyoxylate bypass;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                           Tricarboxylic acid cycle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY SEQUENCE OF 228-250 AND 254-259. MEDLINE-74086945; PubMed-4149369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENZYME REGULATION: INHIBITION OF THIS ENZYME BY PHOSPHORYLATION REGULATES THE BRANCH POINT BETWEEN THE KREBS CYCLE AND THE GLYOXYLATE BYPASS, WHICH IS AN LITERNATE NOUTE THAT ACCUMULATES CARBON FOR BIOSYNVHESIS WHEN ACETATE IS THE SOLE CARBON SOURCE FOR GROWTH. THE PHOSPHORYLATION STATE OF THIS ENZYME IS CONTROLL BY ISCOLTRATE DEHYDROGENASE KINASE/PHOSPHATASE (ACEK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: BELONGS TO THE MONOMERIC-TYPE FAMILY OF IDH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: MONOMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Isocitrate + NADP(+) = 2-oxoglutarate + CO(2)
                                                                                                                                                                                                                                                                DRHMIRMRQLIDIVDQLKNYVNDL-----VPEFLPAPEDVETNCEWSAFSCFQKAQLKS
                                                                                                                                                                       VNPVLREGNSDRRAPLSVKNYARKHP------HKMGAWSADS
                                                                                                                                                                                                                                     DANIIKLPNISASVPQLKAAIKELQQQGYKLPDY---PEEPKTDTEKDVKARYDKIKGSA 133
                                                                                               HUMAN
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                                                                                                                                                                                                                                                                                                  26;
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                                                                                               STANDARD;
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26, Createa)
40, Last sequence update)
41, Last annotation update)
41, Last annotation "like"
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to the EMBL/GenBank/DDBJ
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Pred. No.
                                                                                               PRT;
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RESULT 13
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00225; kinesin; 1. PRINTS; PR00380; KINESINHEAVY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PLUS-END-DIRECTED MOTOR ENZYME THAT MOVES ANTIPARALLEL MICROTUBULES IN VITRO. LOCALIZES TO THE INTERZONE OF MITOTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00411; KINESIN_MOTOR_DOMAIN1; 1. PROSITE; PS50067; KINESIN_MOTOR_DOMAIN2; 1. Motor protein; Cell division; Microtubules;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P33176;
MIM; 605064; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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NCBI_TaxID=9606;
[1]
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Homo sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 359:543-547(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRSSPGNMERIVICLMVIF -- LGTL----VHKSSSQGQDRHMIRMRQLIDIVDQLKNYV
                                                                                                                                                   HQHL---SSRTH 157
                                                                                                                                                                                                                                                         NERIINVSIKKLKRKPPSTNAGRRQK-HRLTCPSCDSYEKKPPKEFLERF--KSLLQKMI 148
                                                                                                                                                                                                                                                                                                            REAMPNPKTSSSKRQVDPEFADMITVQEFCKA-EEVDEDSVYGVFVSY----IEIYNNYI
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856 ;
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Pred. No.
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NUCLEAR LOCALIZATION SIGNAL
ATP (BY SIMILARITY).
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moves antiparallel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Vitellogenin III precursor (Yolk protein 3)
                                                                                                                                      VARIANT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                     PIR;
                                                                                                                                                                                                                                                                                                  EMBL; M15898; AAA29024.1; -. EMBL; X04754; CAA28451.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fertile yolk protein 3 mutant in Drosophila.";
Mol. Gen. Genet. 228:81-88(1991).
-i- FUNCTION: VITELLOCENIN IS THE MAJOR YOLK PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (MUTANT YP3S1)
MEDLINE=91360094; PubMed=1909425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yan Y.L., Kunert C.J., Postlethwait J.H.; "Sequence homologies among the three yolk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87146365; PubMed=3029679;
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                                                                                                                                                                                                                                    FlyBase; FBgn0004047; Yp3.
InterPro; IPR000734; Lipase.
                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic Acids Res. 15:67-85(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                   Yolk; Signal.
                                                                                                                                                                                                                    Pfam; PF00151; lipase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IT IS USED AS A FOOD SOURCE DURING EMBRYOGENESIS.
TISSUE SPECIFICITY: SYNTHESIZED IN THE FAT BODY AND OVARIAN FOLLICLE CELLS AND ACCUMULATE IN THE OCCYTE.
INDUCTION: By beta-ecdysone; in males.
MISCELLANEOUS: THE MUTANT YP3-S1 IS SYNTHESIZED IN THE FAT I BUT NOT SECRETED, PROBABLY DUE TO THE AMINO ACID MUTATION II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL PEPTIDE. SIMILARITY: PARTIAL, TO LIPASES. STRONG TO OTHER VITTELOGENINS
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                            MERIVICLMVIFLGTLVHKSSSQGQDR------HMIRMRQLIDI----
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MMSLRICLLATCLLVAAHASKDASNDRLKPTKWLTATELENVPSLNDITWERLENQPLEQ
                                                                       Similarity
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                                                        Score 76.5; D
Pred. No. 7.4;
L4; Mismatches
                                                                                                                                      VITELLOGENIN III.
A -> D (IN MUTANT YP3S1).
5457C49CAC933B26 CRC64;
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YG3M_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1996 (Rel. 33, Last sequ
16-0CT-2001 (Rel. 40, Last anno
Hypothetical 101.4 kDa protein
YGR150C OR G6642.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Skala J., Nawrocki A., Goffeau A.;
"The sequence of a 27 kb segment on the right arm of chromosome from Saccharomyces cerevisiae reveals MOL1, NAT2, RPL30B, RSR1, PEM1/CHO2, NSR1 genes and ten new open reading frames.";
Yeast 11:1421-1427(1995).
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01-FEB-1996
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EMBL; Z72935; CAA97164.1;
SGD; S0003382; YGR150C.
                                                                                                                                                                                                                                                                                                              Hypothetical
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Pfam; PF01535; PPR; 1.
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                                                                                                                                                                                                                                                                                               SEQUENCE
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151
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AKNLFDRSHSN
                           --HLSSRTHGS
                                                                                   HRLTCPSCDSYEKKPPK - -
                                                                                                                                                                    RCGPKNN---VLCFPFQLSFLFSKRLINK-----RFKYTLQTEDE-KNWMGSLS 49
                                                                                                                                                                                             RSSPGNMERIVIC----LMVIFLGTLVHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLV 57
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                                                       NSIAPISEDSRNVNVTKTSSVPNEEKSKNLSDLIHSSFLEKMDHLVPKVIRERVADDDIL
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43; Conserv
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 161
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33, Last sequence up
40, Last annotation
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22.5%;
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Pred. No. 17;
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RESULT

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ALLA_YEAST
ID ALLA_YEAST
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AC 932459;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ureidoglycolate hydrolase (EC 3.5.3.19).
GN DAL3 OR YIR032C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi: Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Sacc
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-!- FUNCTION: UTILIZATION OF PURINES AS SECONDARY NITROGEN SOURCES, WHEN PRIMARY SOURCES ARE LIMITING.
-!- CATALYTIC ACTIVITY: (-)-ureidoglycolate + H(2)O = glyoxylate + 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 2000 - 
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EMBL; Z38061; CAA86192.1; -.
PIR; S42022; S42022;
PIR; S48494; S48494;
SGD; S0001471; DAL3.
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LIPID 192 192 FARNESYL (BY SIMILARITY).
SEQUENCE 195 AA; 21727 MW; 6230AEE69585206B CRC64;
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"The ureidoglycollate hydrolase (DAL3) gene in Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).

Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetaes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.

NCBI_TaxID=4932;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Yeast 7:693-698(1991).
[2]
                                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 VHKSSSQGQDRHMIRMRQLIDIVDQLKNYVNDLVPEFLPAPEDVETNCEWSAFSCFQKAQ 83 : | ::|| | | ::| | | | ::| | | | ::| | | | ::| | | | ::| | | | ::| | | | | ::| | | | | ::| | | | | ::| | | | | ::| | | | | ::| | | | ::| | | | ::| | | | ::| | | | ::| | | | ::| | | ::| | | | ::| | | ::| | | ::| | | ::| | | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| | ::| 
                                                                                                                                                                                                                                                                                                                                                                                                                                   84 LKSANTGNNERIINVSIKKLKRKPPST 110
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                                                                                                                                                                                                                                                                                                               LNRVFTQGSNQAISHSIKVLEKHPCST 99
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